

Yu, Misook

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Please search SEQ ID NO:68 and DNA encoding SEQ ID NO:68.

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OM protein - protein search, using sw model

Run on: May 19, 2003, 16:31:36 ; Search time 36 Seconds
(without alignments)
869.830 Million cell updates/sec

Title: US-09-847-102a-68

Perfect score: 1310
Sequence: 1 MARPPSAPPSLLLLLAQL.....PNCAPCYQSPFSADERTFA 235

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1310	100.0	585	18	AAW41271
2	824	62.9	694	23	AAU74823
3	823.5	62.9	685	18	AAW31274
4	621	47.4	694	18	AAW31267
5	621	47.4	694	22	ABB71797
6	440.5	33.6	572	18	AAW31273
7	415	31.7	647	21	AAW31217
8	384	29.3	581	22	AAW31308
9	380	29.0	325	19	AAW41767
10	372	28.4	325	19	AAW48695

11	372	28.4	325	19	AAW41254	Human "frizzled" f
12	372	28.4	325	20	AAV03229	Amino acid sequenc
13	372	28.4	325	21	AAW10281	Xenopus sp embryo
14	370.5	28.3	582	22	AAW33307	Mouse frizzled fam
15	370	28.2	589	22	ABW1245	Drosophila melanog
16	367	28.0	323	19	AAW41768	Mouse hnfz protein
17	367	28.0	323	19	AAW41253	Mouse "frizzled" f
18	367	28.0	323	19	ABW57252	Xenopus growth-ind
19	366.5	28.0	319	19	AAW48696	Xenopus growth-ind
20	366	27.9	325	20	AAW48694	Bovine growth-indu
21	366	27.9	325	20	AAV03223	Amino acid sequenc
22	360	27.5	318	19	AAW41251	Xenopus "frizzled"
23	349	26.6	372	22	AAW6347	Partial human FRAZ
24	349	26.1	372	22	AAW48184	Partial amino acid
25	342.5	26.1	346	22	AAW48183	Human FRAZZLED pol
26	342.5	26.1	347	20	AAV03231	Amino acid sequenc
27	342.5	26.1	368	19	AAW73508	Human ARC-1639 pro
28	342.5	26.1	368	20	AAV03232	Full length sequen
29	342	26.1	346	21	AAW33911	Bos taurus Fraxile
30	339.5	25.9	368	20	AAW6346	Human FRAZZLED pro
31	338.5	25.8	346	21	AAW60193	Breast cancer prot
32	338.5	25.8	346	22	AAW6853	Human lung tumour
33	338.5	25.8	346	23	ABG61803	Prostate cancer-as
34	338.5	25.8	346	23	AAW85508	Clone #19118 of lu
35	338.5	25.8	346	23	AAW44432	Human frizzled rel
36	308	23.5	540	21	AAV09093	Human frizzled-4 p
37	304.5	23.2	666	18	AAW31268	Mouse frizzled-4 p
38	299.5	22.9	537	18	AAW31270	Mouse frizzled-4 p
39	299.5	22.9	537	23	ABW57288	Mouse frizzled-4 p
40	297	22.7	338	20	AAV30157	Mouse ischemic co
41	297	22.7	468	22	ABW12060	Amino acid sequenc
42	297	22.7	666	20	AAV30156	Human frizzled-3 h
43	284	21.7	700	22	ABW59309	Amino acid sequenc
44	284	21.7	700	22	ABW59309	Drosophila melanog
45	282	21.5	704	20	AAV02383	Drosophila G-prote

ALIGNMENTS

RESULT 1
AAW31271
ID AAW31271 standard; Protein; 585 AA.
AC AAW31271;
DT 27-APR-1998 (first entry)
XX
DE Human frizzled-5 protein Mfz5-(Mnt-receptor).
XX
KW Mnt receptor; human frizzled-5 protein; Mfz5 gene;
KW signal transduction; cancer; cell growth; cell proliferation.
XX
OS Homo sapiens.
XX
PN W09739357-A1.
XX
PD 23-OCT-1997.
XX
PF 11-APR-1997; 97WO-US06049.
XX
PR 12-APR-1996; 96US-0015307.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
PI Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J;
PI Nusse R, Samos CH, Wangy;
XX
WP1: 1997-526631/48.
DR N-PSDB; AAT89889.
XX
PT Identification of Mnt receptor binding modulators - useful for

PT treatment of cancer and growth, development or proliferation related disorders
 XX
 PS Disclosure; Page 37-39; 61pp; English.
 CC This protein comprises the human transmembrane receptor, CC
 CC frizzled-5 (Hfz5), encoded by the Hfz5 gene (see AAT89889). It is CC
 CC an example of a Wnt receptor. Other novel frizzled family members CC
 CC have been identified in human, mouse and Caenorhabditis elegans CC
 CC (see AAM31268-74) and are considered also to be Wnt receptors. Wnt CC
 CC receptors can be used in a novel, claimed method of screening for CC
 CC compounds which modulate the binding of a Wnt polypeptide (secreted CC
 CC proteins involved in cell-to-cell signalling) to a Wnt receptor. CC
 CC Wnt is involved in (mammary) cancer and other processes involving CC
 CC growth, development and proliferation (both normal and abnormal). CC
 CC Modulators identified by the claimed method are useful for CC
 CC treatment of diseases related to these conditions.
 CC
 XX
 SQ Sequence 585 AA;
 Query Match 100.0%; Score 1310; DB 18; Length 585;
 Best Local Similarity 100.0%; Pred. No. 8.6e-102;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MARPDSPAPSLILLILLALVGRRAAASAPVCOEITVPMCRGIGYNTLHMPNQFNHDTQ 60
 DB 1 MARPDSPAPSLILLILLALVGRRAAASAPVCOEITVPMCRGIGYNTLHMPNQFNHDTQ 60
 QY 61 DEAGLEVHGFVPLVEIQCSBDLRFICTMYTPTICLDYHKPLPPCSVCERAKAGCSPLM 120
 DB 61 DEAGLEVHGFVPLVEIQCSBDLRFICTMYTPTICLDYHKPLPPCSVCERAKAGCSPLM 120
 QY 121 ROYGFAMPMSCDRLPVIGRDAEVLCPMDYNSSEATTAPRPPAPPTLPGPGAPASGG 180
 DB 121 ROYGFAMPMSCDRLPVIGRDAEVLCPMDYNSSEATTAPRPPAPPTLPGPGAPASGG 180
 QY 121 ROYGFAMPMSCDRLPVIGRDAEVLCPMDYNSSEATTAPRPPAPPTLPGPGAPASGG 180
 DB 121 ROYGFAMPMSCDRLPVIGRDAEVLCPMDYNSSEATTAPRPPAPPTLPGPGAPASGG 180
 QY 181 ECPAGGPFVCKCEPFPVPLIKESHPLYNKVRITGOVNCVPCYOPSFADERTFA 235
 DB 181 ECPAGGPFVCKCEPFPVPLIKESHPLYNKVRITGOVNCVPCYOPSFADERTFA 235
 RESULT 2
 AAU74823
 ID AAU74823 standard; protein; 694 AA.
 AC AAU74823;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Human REPTR 6 protein.
 XX
 KW REPTR; human; antiinflammatory; cytostatic; immunosuppressive;
 KW antiviral; anti-HIV; antiarthritic; anticonvulsant; nootropic;
 KW neuroprotective; antiallergic; antibody; immunogen; endometriosis;
 KW gastrointestinal disorder; gastritis; oesophageal carcinoma;
 KW Crohn's disease; irritable bowel syndrome; ulcerative colitis;
 KW endocrine disorder; hypochalimus disorder; Kallman's disease;
 KW autoimmune disease; inflammatory disease; infertility; receptor;
 KW acquired immune deficiency syndrome; AIDS; rheumatoid arthritis;
 KW allergy; osteoarthritis; diabetes mellitus; multiple sclerosis;
 KW systemic lupus erythematosus; cell proliferative disorder;
 KW cancer; developmental disorder; Duchenne muscular dystrophy;
 KW Becker muscular dystrophy; neurological disorder; epilepsy;
 KW Alzheimer's disease; Huntington's disease; reproductive disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200198354-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 21-JUN-2001; 2001WO-US19942.
 XX

PR 21-JUN-2001; 2000US-214027P.
 PR 25-AUG-2000; 2000US-228045P.
 PR 12-DEC-2000; 2000US-255104P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Griffin JA, Kallick DA, Tribouley CM, Yue H, Nguyen DB, Tang YT,
 PI Lal P, Policky JL, Aizawa Y, Lu DM, Graul R, Yao MG, Burford N,
 PI Hafalia AJA, Baughn MR, Bandman O, Patterson C, Yang J, Xu Y;
 PI Gandhi AR, Warren BA, Ding L, Sanjamaal MS, Duggan BM, Lu Y;
 XX
 DR WPI; 2002-090432/12.
 DR N-PDB; ABL15174.
 XX
 PT Twelve human receptors (referred to as REPTR-1 to REPTR-12), useful in
 PT the diagnosis, treatment and prevention of gastrointestinal (e.g.
 PT gastritis), autoimmune/inflammatory (e.g. osteoarthritis) and cell
 PT proliferative (e.g. cancer) disorders -
 XX
 PS Claim 50; Page 119-121; 157pp; English.
 CC
 CC This invention relates to twelve human receptors cDNA sequences
 CC referred to as REPTR-1 to REPTR-12), and the proteins encoded thereby.
 CC The proteins of the invention may have antiinflammatory, cytostatic,
 CC immunosuppressive, antiviral, anti-HIV, antiarthritic, muscular active
 CC general, anticonvulsant, nootropic, neuroprotective, antiallergic
 CC activities. The sequences of the invention may be used to produce REPTR
 CC agonists or antagonists, and the protein sequences may be used to raise
 CC anti-REPTR antibodies. These molecules and the REPTR polynucleotides and
 CC polypeptides of the invention are useful in the diagnosis, treatment and
 CC prevention of gastrointestinal (e.g. gastritis, oesophageal carcinoma,
 CC Crohn's disease, irritable bowel syndrome, ulcerative colitis),
 CC endocrine (e.g. hypochalimus disorder, Kallman's disease), autoimmune/
 CC inflammatory (e.g. acquired immune deficiency syndrome (AIDS),
 CC rheumatoid arthritis, allergies, osteoarthritis, diabetes mellitus,
 CC multiple sclerosis, systemic lupus erythematosus), cell proliferative
 CC (e.g. cancer), developmental (e.g. Duchenne and Becker muscular
 CC dystrophy), neurological (e.g. epilepsy, Alzheimer's disease,
 CC Huntington's disease) and reproductive (e.g. infertility, endometriosis)
 CC disorders. Numerous other examples of each disorder are given in the
 CC specification. The present sequence represents the human REPTR6 protein
 CC sequence of the invention.
 CC
 XX
 SQ Sequence 694 AA;
 Query Match 62.9%; Score 824; DB 23; Length 694;
 Best Local Similarity 59.9%; Pred. No. 6.6e-61;
 Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;
 QY 11 SLL--LTLIAQLVGRRAAASAPVCOEITVPMCRGIGYNTLHMPNQFNHDTQDEAGLEVH 68
 DB 11 SLLAALLQSSGGAASAKELACQETITVPLCKGIGYNTYMPNQFNHDTQDEAGLEVH 70
 QY 69 QFWPLVEIQCSBDLRFICTMYTPTICLDYHKPLPPCSVCERAKAGCSPLMROYGFAMP 128
 DB 71 QFWPLVEIQCSBDLRFICTMYTPTICLDYHKPLPPCSVCERAKAGCAPLMROYGFAMP 130
 QY 129 RMSCDRLPVIGRDAEVLCPMDYNSSEATTAPRPPAPPTLPG-----PPG 174
 DB 131 DMRCDRLPBQ--NBDTLCPMDYNTDLTLTAAPSPRRLLPPP--PGDPPGSGHGRRPG 187
 QY 175 A-----PASG-----ECPAGGPFV-----CKCEPFPVPLIKESH 205
 DB 188 ARPHIRGGGGGGGGAAPAPARGGGGGKARPPGGGAAPBPGQGCAPMVSVSEHNP 247
 QY 206 LYNKVRITGOVNCVPCYOPSFADERTF 234
 DB 248 LYNKVRITGOVNCVPCYOPSFADERTF 276
 RESULT 3
 AAW31274
 ID AAW31274 standard; Protein; 685 AA.

XX AC AAM31274;
XX DT 27-APR-1998 (first entry)
XX DE Mouse frizzled-8 protein Mfz8 (Wnt receptor).
XX KM Wnt receptor; mouse frizzled-8 protein; Mfz8 gene;
XX KM signal transduction; cancer; cell growth; cell proliferation.
XX OS Mus musculus.
XX PN M09739357-A1.
XX PD 23-OCT-1997.
XX PF 11-APR-1997; 97WO-US06049.
XX PR 12-APR-1996; 96US-0015307.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX PI Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J;
XX PI Nusse R, Samos CH, Wangy;
XX DR WPI; 1997-526631/48.
XX DR N-PSDB; AAT89892.
XX PT Identification of Wnt receptor binding modulators - useful for
XX PT treatment of cancer and growth, development or proliferation related
XX PT disorders
XX PS Disclosure; Page 48-50; 61pp; English.
XX CC This protein comprises the mouse transmembrane receptor,
XX CC frizzled-8 (Mfz8), encoded by the Mfz8 gene (see AAT89892). It is
XX CC an example of a Wnt receptor. Other novel frizzled family members
XX CC have been identified in human, mouse and Caenorhabditis elegans
XX CC (see AAM31268-74) and are considered also to be Wnt receptors. Wnt
XX CC receptors can be used in a novel, claimed method of screening for
XX CC compounds which modulate the binding of a Wnt polypeptide (secreted
XX CC proteins involved in cell-to-cell signaling) to a Wnt receptor.
XX CC Wnt is involved in (mammary) cancer and other processes involving
XX CC growth, development and proliferation (both normal and abnormal).
XX CC Modulators identified by the claimed method are useful for
XX CC treatment of diseases related to these conditions.
XX SQ Sequence 685 AA;
Query Match 62.9%; Score 823.5; DB 18; Length 685;
Best Local Similarity 60.0%; Pred. No. 7.2e-61;
Matches 159; Conservative 24; Mismatches 39; Indels 43; Gaps 8;
QY 11 SLV--LILLALVGRAAASAKAPVCQETTPWCRGIGYNTLTHMPNQFHHDTDEAGLEVH 68
DB 11 SLIAALAVLGSSGAAASAKELACQETITVPLCKGIGYNTVMPQFHHDTDEAGLEVH 70
QY 69 QFWPLVEIQCCSPDLRFCTMTPTICLPDYHAKPLPCCSVGERAAAGCSPLMRQYGFAMP 128
DB 71 QFWPLVEIQCCSPDLRFCTMTPTICLPDYHAKPLPCCSVGERAAAGCSPLMRQYGFAMP 130
QY 129 ERMSCDRLPVGRDAEVCMQDNRSEATTA--PPRPPAKPTLGG-----PPG 174
DB 131 DRMRCDRLPEQG-NPDTICMDYNRKIDLTAAASPPRRALPPPPP-PGEGPPSGSGSRPPG 188
QY 175 A-----PASGEC--PAGGPFV---CKRBPFPVILKESHPLYNK 209
DB 189 ARPFRGSSSGSDAAAPSPRGKARPPGGGAAPCEGACCRAPAMTVSVSERRHPLYNR 248
QY 210 VRTGQVPCAVPCYQPSFSDERTF 234
DB 249 VKTGOIANCALPCNHPFSDERRAF 273

RESULT 4
AAM31267
ID AAM31267 standard; Protein; 694 AA.
XX AC AAM31267;
XX DT 27-APR-1998 (first entry)
XX DE Drosophila frizzled-2 protein (Wnt receptor).
XX KM Wnt receptor; Drosophila frizzled-2 protein; Dfz2 gene;
XX KM wingless receptor; Wg receptor; signal transduction; cancer;
XX KM cell growth; cell proliferation.
XX OS Drosophila melanogaster.
XX FH Key Location/Qualifiers
XX FT Misc-difference 268 /note= "encoded by CAC"
XX FT Misc-difference 269 /note= "encoded by TGC"
XX FT Misc-difference 348 /note= "encoded by TGA (apparent 1 nucleotide
XX FT deletion of codon)"
XX FT Misc-difference 488 /note= "encoded by TTA"
XX FT Misc-difference 632 /note= "encoded by CTG"
XX FT Misc-difference 633 /note= "encoded by GCG"
XX FT Misc-difference 671 /note= "encoded by CG (apparent 1 nucleotide
XX FT deletion of codon)"
XX PN W09739357-A1.
XX PD 23-OCT-1997.
XX PF 11-APR-1997; 97WO-US06049.
XX PR 12-APR-1996; 96US-0015307.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX PI Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J;
XX PI Nusse R, Samos CH, Wangy;
XX DR WPI; 1997-526631/48.
XX DR N-PSDB; AAT89885.
XX PT Identification of Wnt receptor binding modulators - useful for
XX PT treatment of cancer and growth, development or proliferation related
XX PT disorders
XX PS Claim 2; Page 23-25; 61pp; English.
XX CC This protein comprises the Drosophila frizzled-2 protein encoded by
XX CC the Dfz2 gene (see AAT89885). It is a receptor for wingless (Wg),
XX CC acting as a signal transducing molecule, and is an example of a Wnt
XX CC receptor (WntR). Other novel frizzled family members have been
XX CC identified in human, mouse and Caenorhabditis elegans (see
XX CC AAM31268-74) and are considered also to be Wnt receptors. Wnt
XX CC receptors can be used in a novel, claimed method of screening for
XX CC compounds which modulate the binding of a Wnt polypeptide (secreted
XX CC proteins involved in cell-to-cell signaling) to a Wnt receptor.
XX CC Wnt is involved in (mammary) cancer and other processes involving
XX CC growth, development and proliferation (both normal and abnormal).
XX CC Modulators identified by the claimed method are useful for
XX CC treatment of diseases related to these conditions.

SQ Sequence 694 AA;
 Query Match 47.4%; Score 621; DB 18; Length 694;
 Best Local Similarity 43.4%; Pred. No. 7.3e-44;
 Matches 124; Conservative 27; Mismatches 55; Indels 80; Gaps 7;

QY 22 GRAAASKAP-----VCEITVPMCRGIGYNTLTHMPNQFNHDTODEAGLEVH 68
 DB 40 GHGLDASPAPGVPAIPKDPNLRCEIITIPMCRGIGYNTSPFNHMTODEAGLEVH 99
 QY 69 QFWPLVEIKCSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCERAYAGCSPLMROYGFAMP 128
 DB 100 QFWPLVEIKCSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCERAYAGCSPLMROYGFAMP 159
 QY 129 ERMSCDRLPLVGRDAEVLICMDY----- 150
 DB 160 ERMACEHLPLHG-DPDNLCMEQPSYTEAGSGSGSGSGSGSGGKRGKOGSGSGGS 218
 QY 151 ----NRSEATTAPRPFPAPKPTLPGPGAPASGCECPAGGPFVCKCREPPV----- 197
 DB 219 GAGSGSGSTSTPCRGGRNSK-NCONPQGEKASGKECS-----CSCRSPLIPLGKEQLIQ 271
 QY 198 -----PIKESHPLYNKV---RTGOVPCAVPCYOPSPFSADERTFA 235
 DB 272 QOSQPMHMHPPHMYMNLTVQRIAGVPNCGIPLCKGPFPSNDEKQFA 317

RESULT 5
 ABB71797
 ID ABB71797 standard; Protein; 694 AA.
 AC ABB71797;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 42183.
 XX
 KM Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmaceutical.
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 XX
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 DR WPI; 2001-656660/75.
 DR N-PSDB; ABL15900.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 XX Disclosure; SEQ ID NO 42183; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB5737-ABB72072).
 CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_ptc_sequences.
 CC
 SQ Sequence 694 AA;
 Query Match 47.4%; Score 621; DB 22; Length 694;
 Best Local Similarity 43.4%; Pred. No. 7.3e-44;
 Matches 124; Conservative 27; Mismatches 55; Indels 80; Gaps 7;

QY 22 GRAAASKAP-----VCEITVPMCRGIGYNTLTHMPNQFNHDTODEAGLEVH 68
 DB 40 GHGLDASPAPGVPAIPKDPNLRCEIITIPMCRGIGYNTSPFNHMTODEAGLEVH 99
 QY 69 QFWPLVEIKCSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCERAYAGCSPLMROYGFAMP 128
 DB 100 QFWPLVEIKCSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCERAYAGCSPLMROYGFAMP 159
 QY 129 ERMSCDRLPLVGRDAEVLICMDY----- 150
 DB 160 ERMACEHLPLHG-DPDNLCMEQPSYTEAGSGSGSGSGSGSGGKRGKOGSGSGGS 218
 QY 151 ----NRSEATTAPRPFPAPKPTLPGPGAPASGCECPAGGPFVCKCREPPV----- 197
 DB 219 GAGSGSGSTSTPCRGGRNSK-NCONPQGEKASGKECS-----CSCRSPLIPLGKEQLIQ 271
 QY 198 -----PIKESHPLYNKV---RTGOVPCAVPCYOPSPFSADERTFA 235
 DB 272 QOSQPMHMHPPHMYMNLTVQRIAGVPNCGIPLCKGPFPSNDEKQFA 317

RESULT 6
 AAW31273
 ID AAW31273 standard; Protein; 572 AA.
 AC AAW31273;
 XX
 DT 27-APR-1998 (first entry)
 XX
 DE Mouse frizzled-7 protein Mfz7 (Wnt receptor).
 XX
 KM Wnt receptor; mouse frizzled-7 protein; Mfz7 gene;
 XX signal transduction; cancer; cell growth; cell proliferation.
 XX
 OS Mus musculus.
 XX
 PN M09739357-A1.
 XX
 PD 23-OCT-1997.
 XX
 PF 11-APR-1997; 97WO-US06049.
 XX
 PR 12-APR-1996; 96US-0015307.
 XX
 PA (UYUO) UNIV JOHNS HOPKINS.
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J;
 DR WPI; 1997-526631/48.
 DR N-PSDB; AAT89891.
 XX
 PT Identification of Wnt receptor binding modulators - useful for
 PT treatment of cancer and growth, development or proliferation related
 PT disorders
 XX
 XX Disclosure; Page 44-46; 61pp; English.
 XX
 CC This protein comprises the mouse transmembrane receptor,
 CC frizzled-7 (Mfz7), encoded by the Mfz7 gene (see AAT89891). It is
 CC an example of a Wnt receptor. Other novel frizzled family members
 CC have been identified in human, mouse and Caenorhabditis elegans
 CC (see AAW31268-74) and are considered also to be Wnt receptors. Wnt

CC receptors can be used in a novel, claimed method of screening for
CC compounds which modulate the binding of a wt polypeptide (secreted
CC proteins involved in cell-to-cell signalling) to a wt receptor.
CC Mtt is involved in (mammary) cancer and other processes involving
CC growth, development and proliferation (both normal and abnormal).
CC Modulators identified by the claimed method are useful for
CC treatment of diseases related to these conditions.

XX Sequence 572 AA;

Query Match 33.6%; Score 440.5; DB 18; Length 572;
Best Local Similarity 38.8%; Pred. No. 8.4e-29;
Matches 100; Conservative 36; Mismatches 75; Indels 47; Gaps 12;

QY 8 APPLLLLLLALQVRAAASKAP-----VCOEITVPMCRGIGYVLTMPN 53
DB 11 SPDLCLALVLA-LGALPTDRAQPHYGEKGISVDPHFCPPISLPTCTDAIQTIIIPN 69
QY 54 QFNHDQDEAGLEVHGFMPVLEIQCSPDLRFELCTMTYTPICLPYHKPLPCRSVCERAK 113
DB 70 LIGHTNEDAGLEVHGFYPLVYKQCSPELRFELCSMYAPVCTV-LDQALPPCRSLCERAR 128
QY 114 AGCEPLMROVGFAMPBENSCRLPYLGRDAVLCMDYRSEAT--TAPRPPPAKPTLP 170
DB 129 QGCEALNNKFGFQWPERLRCEHPVHG--AGEICVGQNTSDSGAGSPYAPYAPLP 186
QY 171 GPPGAPASGCECPAGC-----PFVCKCRPEFVPLIKESHPLVYKVRGTGVNCAVPCYQ 224
DB 187 DPEPTAMS-----PSDGKRLSPFSCF-RQLKVP-----PYLGRFLGE-RDGCAPC-E 233
QY 225 PS-----PSADERTFA 235
DB 234 PGRANGLMYFKEBERRFA 251

RESULT 7
AAB12117
ID AAB12117 standard; Protein; 647 AA.

XX AAB12117;

DT 02-FEB-2001 (first entry)

XX Hydrophobic domain protein from clone HP02539 isolated from Saos-2 cells.

XX Human: secreted protein; membrane protein; hydrophobic domain;
XX proliferation control; differentiation induction; material transport;
XX biophysics; signal receptor; ion channel; transporter; immunostimulant;
XX immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic;
XX haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
XX autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer.

XX Homo sapiens.

XX WO200029448-A2.

XX 25-MAY-2000.

XX 17-NOV-1999; 99WO-JP06412.

XX 17-NOV-1998; 98JP-0326255.

XX 22-DEC-1998; 98JP-0364315.

XX 16-MAR-1999; 99JP-0069811.

XX 27-APR-1999; 99JP-0119289.

XX 19-MAY-1999; 99JP-0138169.

XX (SAGA) SAGAMI CHEM RES CENT.

XX (PROT-) PROTEGENE INC.

XX Kato S, Kimura T;

XX WPI, 2000-387753/33.

XX N-PSDB; AAA60179, AAA60189.

XX Proteins comprising hydrophobic regions, such as secretory and membrane
XX proteins, useful in research and diagnostics and having various
XX activities e.g. immunomodulatory, antiinflammatory, chemokinetic,
XX hemostatic, thrombolytic -
XX Claim 1; Page 178-181, 410pp; English.

CC Secretory proteins play important roles in the proliferation control, the
CC differentiation induction, the material transport and the biophysics of
CC cells. Membrane proteins have important roles as signal receptors, ion
CC channels and transporters. The present sequence is a human protein which
CC has at least one hydrophobic domain. This protein may be a secretory or a
CC membrane protein. The present protein may have stimulating or suppressing
CC proliferation/differentiation activity, immune stimulating or suppressing
CC activity, haematopoiesis activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, anti-inflammatory activity and tumour
CC inhibition activity. The present protein could therefore be used for
CC treatment of autoimmune disease, Alzheimer's disease, Parkinson's
CC disease, and cancer.

XX Sequence 647 AA;

Query Match 31.7%; Score 415; DB 21; Length 647;
Best Local Similarity 36.0%; Pred. No. 1.3e-26;
Matches 104; Conservative 30; Mismatches 87; Indels 68; Gaps 11;

QY 3 RP-DPSAPSLILLI-----AOLVG-RAAASKAP----- 31
DB 43 RPPVDPRLARQLLLMLLEAPLLGLVRAQAAGCGGCGPQQPPPPQOQSGQY 102
QY 32 -----VCOEITVPMCRGIGYVLTMPNQFNHDQDEAGLEVHGFMPVLEIQC 79
DB 103 NGERGISVDPHFCPPISLPTCTDAIQTIIIPNLTGHTNEDAGLEVHGFYPLVYKQCS 162
QY 80 PDLRFELCTMTYTPICLPDYHKPLPCRSVCERAKAGCSPMLROYGFAMPBENSCRLPYL 139
DB 163 AELKFFLCMYAPVCTV-LDQALPPCRSLCERARQCEALNNKFGFQWPDILKCEKRPVH 221
QY 140 GRDAEVLICMDYRSEATTAAPRPPPAKPTLPGPPGAPASGCECPAG-----GPFVCKCR 193
DB 222 G--AGEICVGQNTSDKQTPPRLPEFWTSNPQHGSGHGGPFGAGAGASBRGKFCF-R 278
QY 194 EPPVPLIKESHPLVYKVRGTGVNCAVPCYQPS-----PSADERTFA 235
DB 279 ALKVPSTLYNHYFGEK-----DCGAPC-EPTKVGLMYFGPELRFS 319

RESULT 8
AAB73308
ID AAB73308 standard; Protein; 581 AA.

XX AAB73308;

DT 22-MAY-2001 (first entry)

XX Human frizzled family protein 584.

XX Human: frizzled family gene 584; embryo; foetus; cancer;
XX drug discovery; cytostatic.

XX Homo sapiens.

XX WO200112808-A1.

XX 22-FEB-2001.

XX 18-AUG-2000; 2000WO-JP05552.

XX 18-AUG-1999; 99JP-0232018.

XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Senoo C, Numata M;
 XX WPI; 2001-211220/21.
 DR N-PSDB; AAF75974.
 XX Novel frizzled family genes 584 strongly expressed in embryo and fetus
 PT as well as in cancer cells; useful in drug development for diseases
 PT with abnormal expression including tumor
 XX
 PS Claim 1; Fig 6-7; 89pp; Japanese.
 XX The invention relates to a novel frizzled family gene, 584, from mouse
 CC and human (CDNAs given in AAF75973 and AAF75974), and to the mouse and
 CC human 584 proteins (AAF73307, AAF73308). Gene 584 is strongly expressed
 CC in the embryo and foetus, and is also strongly expressed in cancer
 CC cells. The invention also relates to recombinant vectors and host
 CC cells comprising gene 584 nucleic acids, the recombinant expression of
 CC the 584 protein, methods of screening for modulators of 584 activity or
 CC expression, and the compounds thus identified. The human and mouse 584
 CC genes represent a novel gene target for the development of drugs useful
 CC in the treatment of diseases such as cancer. The present sequence
 CC represents human protein 584.
 CC
 SO Sequence 581 AA;
 Query Match 29.3%; Score 384; DB 22; Length 581;
 Best Local Similarity 39.6%; Pred. No. 4,8e-24;
 Matches 82; Conservative 27; Mismatches 70; Indels 28; Gaps 7;
 QY 1 MARPPSAAPSLILLILLLAOLVGRAAAASKAPV-----COEITVPMCRGIGYLTMPN 53
 DB 1 MORPSPR-----LMLVLVQVMGSCAIISSMDMERPGDKCQPIELIMCKDIGYNTMPN 54
 QY 54 QENHTOBEAGLEVQOFMPLVEIQSPDLRFELCTMTPTICLPDYHKPLPCRSVCERAK 113
 DB 55 LMGHNNORAAIQLHEFAPLVYGGHLPFLCSLYAMCTEQVSTPIACRWCEQAR 114
 QY 114 AGCSPLMROYGFAPWBERMSCDRLPVILGRDAEVLCDM--YNRSEATY-----APPR 161
 DB 115 LKCSPIMEQFNFKWPDSDLCRKL-P-NKNDPNYLCEAPNNGSDEPTRSGLPPLPRPQR 173
 QY 162 PPPAKPTLPFGPAPASGGECPAGGPF 188
 DB 174 PHSAQEH-PLKDGPGRGG-CDNPGKF 198
 RESULT 9
 AAW41767
 ID AAW41767 standard; Protein; 325 AA.
 XX AAW41767;
 AC
 XX 28-SEP-1998 (first entry).
 DT
 XX Human hsfz protein.
 DE
 XX Human; nerve cell growth factor; hsfz protein; neuronal cell;
 KM proliferation; differentiation factor.
 KM
 OS Homo sapiens.
 OS DE19702835-A1.
 PN
 XX 22-JAN-1998.
 PD
 XX 27-JAN-1997; 97DE-1002835.
 PF
 XX 09-JUL-1996; 96DE-1027631.
 PR
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Deutsch U. Drexler JCA, Lottspeich F, Mayr T, Riseu W;

PI Rohrer H;
 XX WPI; 1998-088096/09.
 DR N-PSDB; AAV13101.
 XX New nucleic acid encoding protein that increases neuronal cell
 PT proliferation - useful as nerve growth factor and for detection or
 PT inhibition of differentiation factors
 XX
 PS Claim 5; Page 17; 27pp; German.
 XX This sequence represents the human hsfz protein. This protein is found to
 CC increase the proliferation of neuronal cells. Such proteins can be used
 CC as nerve cell growth factors and for the detection and/or inhibition of
 CC differentiation factors, specifically those corresponding to the
 CC Drosophila melanogaster wingless or mouse int-1 type.
 CC
 SO Sequence 325 AA;
 Query Match 29.0%; Score 380; DB 19; Length 325;
 Best Local Similarity 36.0%; Pred. No. 5,4e-24;
 Matches 81; Conservative 34; Mismatches 80; Indels 30; Gaps 7;
 QY 10 PSLILLILLLAOLVGRAA-----AASKAPVCOEITVPMCRGIGYLTMPNPNHTQDEA 63
 DB 6 PGMILLRAGLLAALCLLRVPARAAACEPVRIPLCKSLPMWMTKMPNLIHSTQDNA 65
 QY 64 GLEVHQFMPVLEIQSPDLRFELCTMTPTICLPDY-HKPLPCCRSGVERAKAGCSPLMRQ 122
 DB 66 ILAIHQFEGGLGTHCSFDLFLFCAMTAPICTIDPOHEPIPCSSVCERARQCEPIIHK 125
 QY 123 YGFAPWBERMSCDRLPVILGRDAEVLCDMYNRSEATYAPPPPAKPTLPFGPAPASGSEC 182
 DB 126 YRHSWPENLACEELPVYDRG---VCI--SPEAIVTADGADPP-----MDSNGNC 170
 QY 183 PAGEDFVCKREPFVPIIKESHPL-----YNKVRIGQVPCNCAVPCY 223
 DB 171 RGASSERCKCK---PIRATQKTYFRNNYVIRAKVKEIKTKCH 211
 RESULT 10
 AAW48695
 ID AAW48695 standard; Protein; 325 AA.
 XX AAW48695;
 AC
 XX 04-SEP-1998 (first entry)
 DT
 XX Human growth-inducing protein Frzb sequence.
 DE
 XX Frzb; growth-inducing protein; bovine; human; Xenopus; cartilage;
 KW bone; nerve; muscle; tumour; Wnt-expressing tumour; myoderegulation;
 KW subglottic stenosis; chondromalacia patellae; osteoarthritis;
 KW joint surface lesion; neurodegeneration; Alzheimer's disease;
 KW osteodegeneration; angiogenesis; wound healing.
 KW
 XX Homo sapiens.
 OS
 XX WO9816641-A1.
 PN
 XX 23-APR-1998.
 PD
 XX 08-OCT-1997; 97WO-US18362.
 PF
 XX 20-MAR-1997; 97US-0822333.
 PR
 XX 11-OCT-1996; 96US-0729452.
 PR
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Hoang B, Luyten FP, Moos M, Wang S;
 XX WPI; 1998-251288/22.
 DR N-PSDB; AAV18254.

XX New nucleic acid encoding human, bovine and Xenopus Frzb protein -
PT and related proteins, antibodies, peptide(s), vectors and
PT transformed cells, used to induce growth of cartilage, bone, nerve
PT and muscle, also for inhibiting Wnt-expressing tumours
XX
XX Claim 4, Pages 37-38; 66pp; English.

XX This represents a human growth-inducing protein Frzb. Bovine, human
CC and Xenopus Frzb genes which are shown in AAV18253 to AAV18255 are
CC related to the frizzled gene in Drosophila. The corresponding bovine,
CC human and Xenopus Frzb protein sequences are shown in AAV48694 to
CC AAV48696. A recombinant construct containing a Frzb encoding nucleic acid
CC linked to a heterologous promoter in an expression vector can be used to
CC produce recombinant Frzb proteins. The Frzb proteins may be formulated
CC with fibrin glue, freeze-dried cartilage grafts or collagen (optionally
CC also cartilage progenitor cells, chondroblasts or chondrocytes). They
CC are coated on to, or mixed with, a (non-)resorbable matrix, or mixed with
CC a biodegradable polymer. They modulate activity of the growth factors
CC Wnt-1 to 8. The Frzb proteins induce skeletal morphogenesis, embryonic
CC pattern formation and tissue specificity and are used to induce growth
CC of cartilage, bone, nerve and muscle, particularly in cases of
CC subglottic stenosis, chondromalacia patellae, osteoarthritis, joint
CC surface lesions, neurodegeneration (e.g. Alzheimer's disease),
CC myodegeneration or osteodegeneration. They also modulate Wnt-mediated
CC signalling in cells, and are used to inhibit growth of Wnt-expressing
CC tumours (particularly mammary or intestinal). The Frzb genes may also be
CC used to identify specific modulators or as a growth factor for cells of
CC the chondrocyte lineage in vitro, to stimulate wound healing, to promote
CC angiogenesis, to prevent transplant rejection and as adjunct to
CC chemotherapy or immunotherapy. Fragments of Frzb proteins are used for
CC detecting genetic abnormalities associated with Frzb genes.

XX Sequence 325 AA;

Query Match 28.4%; Score 372; DB 19; Length 325;
Best Local Similarity 35.6%; Pred. No. 2.6e-23;
Matches 80; Conservative 34; Mismatches 81; Indels 30; Gaps 7;

10 PSLILLIAOLVGRRA-----AASKAPVCOEITVPMCRGIVNLTMPNPNHDTODEA 63
Db 6 PGGMLLRAGLALALALCLLVPGARAACEPRVIRPLCKSLPMWMTKPNHLHSTQANA 65
Qy 64 GLEVHOEPLVEIQCSPDLRFELCTMTYPICLPDY-HKPLPPCRSVCEERAKAGCSPLMRQ 122
Db 66 ILAIEQFEGGLGTHCSDDLFLFLCAMYAPICITIDFQHEPIRCKSVCEERAKAGCEPIIIRK 125
Qy 123 YGFAMPERMSCDRLPVLRDAEVLQMDYNRSEATTAPRPPAKPTLPGPGAPASGSEC 182
Db 126 YRHSWPEMLACEELPVYDRG---VCI--SPEAIVTADGADFP-----MDSNGNC 170
Qy 183 PAGGFVCKCEPRFVPIIKESHPL-----YKNVRCQVPCNCAVPCY 223
Db 171 RGASSERCKK---PIRATOKTYFRNNYVIRAKVKEIKTKCH 211

RESULT 11
AAW41254
ID AAW41254 standard; Protein; 325 AA.

XX AAW41254;
XX
XX 09-JUL-1998 (first entry)
XX
XX Human "frazzled" frzb-1.
XX
XX Growth factor; frazzled; frzb-1; Wnts antagonist; human;
KM tumour suppressor; cancer.
XX
XX Homo sapiens.
XX
XX W09748275-A1.
XX

PD 24-DEC-1997.
XX
XX 19-JUN-1997; 97WO-US10942.
PF
XX 18-JUN-1997; 97US-0878474.
PR
XX 20-JUN-1996; 96US-0020150.
XX
XX (REGC) UNIV CALIFORNIA.
PA
XX
XX Boummeester T, De Robertis EM;
PI
XX WPI, 1998-062760/06.
DR
XX N-PSDB; AAV14017.
DR

XX New isolated growth factors - with neurotrophic, growth or
PT differentiation factor activity, tumour growth suppressor activity
PT or mesoderm differentiation activity
XX
XX Claim 6; Fig 9; 48pp; English.

XX The present sequence is the human growth factor protein
CC "frazzled" frzb-1. frzb-1 is an antagonist of Wnts in vivo, and
CC thus is believed to find utility as a tumour suppressor gene,
CC since overexpressed Wnt proteins cause cancer. Frzb-1 may also be a
CC useful vehicle for solubilisation and therapeutic delivery of
CC complexed Wnt proteins.

XX Sequence 325 AA;

Query Match 28.4%; Score 372; DB 19; Length 325;
Best Local Similarity 35.6%; Pred. No. 2.6e-23;
Matches 80; Conservative 34; Mismatches 81; Indels 30; Gaps 7;

Qy 10 PSLILLIAOLVGRRA-----AASKAPVCOEITVPMCRGIVNLTMPNPNHDTODEA 63
Db 6 PGGMLLRAGLALALALCLLVPGARAACEPRVIRPLCKSLPMWMTKPNHLHSTQANA 65
Qy 64 GLEVHOEPLVEIQCSPDLRFELCTMTYPICLPDY-HKPLPPCRSVCEERAKAGCSPLMRQ 122
Db 66 ILAIEQFEGGLGTHCSDDLFLFLCAMYAPICITIDFQHEPIRCKSVCEERAKAGCEPIIIRK 125
Qy 123 YGFAMPERMSCDRLPVLRDAEVLQMDYNRSEATTAPRPPAKPTLPGPGAPASGSEC 182
Db 126 YRHSWPEMLACEELPVYDRG---VCI--SPEAIVTADGADFP-----MDSNGNC 170
Qy 183 PAGGFVCKCEPRFVPIIKESHPL-----YKNVRCQVPCNCAVPCY 223
Db 171 RGASSERCKK---PIRATOKTYFRNNYVIRAKVKEIKTKCH 211

RESULT 12
AAV03229
ID AAV03229 standard; Protein; 325 AA.

XX AAV03229;
XX
XX 03-AUG-1999 (first entry)
XX
XX Amino acid sequence of Xenopus clone WA129_21.
XX
XX Xenopus; clone WA129_21; embryo cDNA library; vaccine;
KM nutrition; cytokine; cell proliferation; cell differentiation;
KM immune stimulating; suppression; haematopoiesis; activin; inhibin;
KM chemotactic; chemokine; haemostatic; thrombolytic; cadherin;
KM anti-inflammatory; tumour invasion suppressor; tumour inhibition.
XX
XX Xenopus sp.
XX
XX W09909061-A1.
XX
XX 25-FEB-1999.
XX
XX 21-AUG-1998; 98WO-US17469.
PF

XX 20-AUG-1998; 98US-0137226.
 PR 21-AUG-1997; 97US-0916041.
 XX
 PA (GEMV) GENETICS INST INC.
 XX
 PI Evans C, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
 PI Racie LA, Treacy M;
 XX WPI: 1999-190151/16.
 DR N-PSDB; AAX28653.
 XX
 PT New polynucleotides encoding secreted proteins - derived from, e.g.
 PT human fetal kidney, potentially useful as vaccines
 XX
 PS Claim 12; Pages 69-70; 75pp; English.
 CC
 CC This is the amino acid sequence of the clone WA129_2i isolated
 CC from Xenopus embryo cDNA library, which has a potential use
 CC as a vaccine. The nucleotides and proteins are predicted to have
 CC biological activities which would make them suitable for treating,
 CC preventing or ameliorating medical conditions in humans and animals,
 CC although no supporting data is given. Suggested activities include
 CC nutritional activity, cytokine and cell proliferation/differentiation
 CC activity, immune stimulating (e.g. as vaccines) or suppressing
 CC activity, haematopoiesis regulating activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity,
 CC haemostatic and thrombolytic activity, receptor/ligand activity,
 CC anti-inflammatory activity, cadherin/tumour invasion suppressor
 CC activity, and tumour inhibition activity. The nucleotides are also
 CC stated to be useful for gene therapy.
 CC
 SQ Sequence 325 AA;

Query Match 28.4%; Score 372; DB 20; Length 325;
 Best Local Similarity 35.6%; Pred. No. 2.6e-23;
 Matches 80; Conservative 34; Mismatches 81; Indels 30; Gaps 7;

OY 10 PSLILLLLAOLVGRRA-----AASKAPVCOEITVPMCRGIGVNLTHMPNOFNHDTODEA 63
 Db 6 POGMILLRAGLLAALACLRVPGARAACEPVRIPLCKSLPMNMTKRNHLHHSTQANA 65
 OY 64 GLEVHQFWPLVEIQSPDLRFELCTMTYPTICLPDY-HKPLPPCRSVCEERAKAGCSPLMRQ 122
 Db 66 ILAIQFEGILGTHCSPLDLFFLCAMVAPICTIDFQHEBIRKCKSVCEERARQGCSEPIILIK 125
 OY 123 YGFAPPEMNSCDRLPYLGRDAVLCMDYNSRATTAAPRPFPAPKPTLPGPAPASGSEC 182
 Db 126 YRHSPENLACEELPVYDRG---VCI--SPEAIVTADGADFP-----MDSSNGNC 170
 OY 183 PAGGFVCKCREPFVPILEKESHPL-----YNKVRTGOVPCAVPCY 223
 Db 171 RGASSERCKCK-----PIRATOKTYFRNNYNYVIRAKVEIKTKCH 211

RESULT 13
 AAB10281
 ID AAB10281 standard; Protein: 325 AA.
 XX
 AC AAB10281;
 XX
 DT 16-NOV-2000 (first entry)
 XX
 DE Xenopus sp embryo protein fragment WA129_1i.
 XX
 KM Secreted protein; cyostatic; immunostimulatory; antimicrobial;
 KM antiviral; immunosuppressive; antiinflammatory; vulnery; cytokine;
 KM cell proliferation; differentiation; regulatory; treatment; tumor;
 KM autoimmune disease; inflammatory disorder; wound; microbial infection;
 KM viral disease; graft versus host reaction suppression.
 XX
 OS Xenopus sp..
 XX

PN WO200037630-A1.
 XX
 XX 29-JUN-2000.
 PD
 XX
 XX 22-DEC-1999; 99WO-US31005.
 PF
 XX
 PR 23-DEC-1998; 98US-0220876.
 XX
 XX
 PA (GEMV) GENETICS INST INC.
 XX
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Bowman MR;
 XX WPI: 2000-442661/38.
 DR N-PSDB; AAA40573.
 XX
 PT Secreted human proteins AS296-1i and AS34-1i, useful for treating
 PT tumors, autoimmune diseases, inflammatory disorders, wounds, microbial
 PT infections and viral diseases -
 XX
 PS Disclosure; Page 280-281; 293pp; English.
 CC
 CC This invention describes novel secreted human proteins (I) which have
 CC cyostatic, immunostimulatory, antimicrobial, antiviral,
 CC immunosuppressive, antiinflammatory and vulnery activity and which act
 CC as cytokine, cell proliferation or differentiation regulators. (I)
 CC is useful for treating tumors, autoimmune diseases, inflammatory
 CC disorders, wounds, microbial infections and viral diseases. (I) is also
 CC useful for suppressing graft versus host reaction. AAB10226-B10288
 CC represent the secreted proteins encoded by AAA40490-A40580 which are
 CC described in the method of the invention.
 CC
 SQ Sequence 325 AA;

Query Match 28.4%; Score 372; DB 21; Length 325;
 Best Local Similarity 35.6%; Pred. No. 2.6e-23;
 Matches 80; Conservative 34; Mismatches 81; Indels 30; Gaps 7;

OY 10 PSLILLLLAOLVGRRA-----AASKAPVCOEITVPMCRGIGVNLTHMPNOFNHDTODEA 63
 Db 6 POGMILLRAGLLAALACLRVPGARAACEPVRIPLCKSLPMNMTKRNHLHHSTQANA 65
 OY 64 GLEVHQFWPLVEIQSPDLRFELCTMTYPTICLPDY-HKPLPPCRSVCEERAKAGCSPLMRQ 122
 Db 66 ILAIQFEGILGTHCSPLDLFFLCAMVAPICTIDFQHEBIRKCKSVCEERARQGCSEPIILIK 125
 OY 123 YGFAPPEMNSCDRLPYLGRDAVLCMDYNSRATTAAPRPFPAPKPTLPGPAPASGSEC 182
 Db 126 YRHSPENLACEELPVYDRG---VCI--SPEAIVTADGADFP-----MDSSNGNC 170
 OY 183 PAGGFVCKCREPFVPILEKESHPL-----YNKVRTGOVPCAVPCY 223
 Db 171 RGASSERCKCK-----PIRATOKTYFRNNYNYVIRAKVEIKTKCH 211

RESULT 14
 AAB73307
 ID AAB73307 standard; Protein: 582 AA.
 XX
 AC AAB73307;
 XX
 DT 22-MAY-2001 (first entry)
 XX
 DE Mouse frizzled family protein 584.
 XX
 KM Mouse; murine; frizzled family gene 584; embryo; foetus; cancer;
 KM drug discovery; cyostatic.
 KM
 OS Mus musculus.
 XX
 PN WO200112808-A1.
 XX
 PD 22-FEB-2001.

XX 18-AUG-2000; 2000WO-JP05552.
PF
XX 18-AUG-1999; 99JP-0232018.
PR
XX (CHUGAI) CHUGAI RES INST MOLECULAR MEDICINE INC.
PA
XX Senoo C, Numata M;
PI
XX WPI; 2001-211220/21.
DR
XX N-PSDB; AAF75973.
PT Novel frizzled family genes 584 strongly expressed in embryo and fetus
PT as well as in cancer cells; useful in drug development for diseases
PT with abnormal expression including tumor -
XX
XX PS Claim 1; Fig 1; 89pp; Japanese.
XX
XX The invention relates to a novel frizzled family gene, 584, from mouse
CC and human (cDNAs given in AAF75973 and AAF75974), and to the mouse and
CC human 584 proteins (AAF7307, AAF7308). Gene 584 is strongly expressed
CC in the embryo and foetus, and is also strongly expressed in cancer
CC cells. The invention also relates to recombinant vectors and host
CC cells comprising gene 584 nucleic acids; the recombinant expression of
CC the 584 protein, methods of screening for modulators of 584 activity or
CC expression, and the compounds thus identified. The human and mouse 584
CC genes represent a novel gene target for the development of drugs useful
CC in the treatment of diseases such as cancer. The present sequence
CC represents mouse protein 584.
XX
SQ Sequence 582 AA;
Query Match 28.3%; Score 370.5; DB 22; Length 582;
Best Local Similarity 34.9%; Pred. No. 6.5e-23;
Matches 87; Conservative 34; Mismatches 93; Indels 35; Gaps 10;
QY 1 MARPPSAPPSLLILLALQVGRRAAASKAPV-----COEITVPMCRGIGYNTLTMNP 53
DB 1 MOHPFPR-----LMLVLQVMIGSCTAISMDLERPDGCGVEIIPMCKDIGYNTTMRPN 55
QY 54 QFNHDTQDAGLEVNQFPLVEIQSPDLRFCTMTYPICLPDYHKLPPRSCERAK 113
DB 56 LMGNHNGEALAIQLHEFAPLVEYGHSLRFPLCSLYAPMCTEQYSTPIACRVNCEQAR 115
QY 114 AGCSPLMQYGFAMPBRASCDRLPVLGRDAEVLQMD--YNRSEATTAPRPPAKPTLP 171
DB 116 LKCSIMQFRRWPSDLSCKLP-NKNDPNTLCMEAPNNGSDSRSGMFP--PLP-- 170
QY 172 PPGAPASGGECPA--GGPFVCKCREPFVPIKESHPLYNKVTGTQVPCA--VPCYOPS 226
DB 171 RPRPHSAQEHPLKDGCGRAGCDNP-----GKFNHVEKSE--SCAPLCTGTGVVY 219
QY 227 FSADERTFA 235
DB 220 WSRDCKRA 228
RESULT 15
ABB71245
ID ABB71245 standard; Protein, 589 AA.
XX
XX ABB71245;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX Drosophila melanogaster polypeptide SEQ ID NO 40527.
DE
XX Drosophila melanogaster polypeptide SEQ ID NO 40527.
KW
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
OS
XX Drosophila melanogaster.
XX
FN W0200171042-A2.

XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US09231.
XX
XX PF 23-MAR-2000; 2000US-191637P.
XX
XX PR 11-JUL-2000; 2000US-0614150.
XX
XX PA (PEKE) PE CORP NY.
XX
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
DR
XX N-PSDB; ABL15348.
PT
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX PS Disclosure; SEQ ID NO 40527; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL10511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 589 AA;
Query Match 28.2%; Score 370; DB 22; Length 589;
Best Local Similarity 40.9%; Pred. No. 7.2e-23;
Matches 85; Conservative 29; Mismatches 72; Indels 22; Gaps 9;
QY 33 COEITVPMCRGIGYNTLTMNPQFNHDTQDAGLEVNQFPLVEIQSPDLRFPLCTMYTP 92
DB 53 CEPITISTCKNIPYNTMTMPNLIGHTKQENGLVEVQFAPLVKIGSDLDLPFLCSLYP 112
QY 93 ICLPDYHKLPLPCRSVCERAKAGCSPLMROYGFAMPBRMSCDRLPVLGRDAEVLQMDYN- 151
DB 113 VCTILERPPIPCSLCESARV-CEKLMKTYNFMFPEULBESKRPVNG--GEDLCVAENT 168
QY 152 -RSEATTAPRPPAKPTLPGPAPASGGECPAGG--PFVCKCREPFVPI-LKESHPLYN 208
DB 169 TSSASTATPTRSVAKVT---TRKHQGVESPHRNIGFVC-----PVQLKTPPLGMGY 217
QY 209 KVRTG---QVNCAPVPCQPSFADERT 233
DB 218 ELKVGKQDLHDGAPCHAMFFPRERT 245

Search completed: May 19, 2003, 16:34:12
Job time : 39 secs

GenCore version 5.1.4 p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2003, 16:33:37 ; Search time 15 Seconds
(without alignments)
460,959 Million cell updates/sec

Title: US-09-847-102a-68
Perfect score: 1310
Sequence: 1 MARPPSPAPSLLLLLLAQL.....PNCAPCYPSFSADERTFA 235

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents AA.*
2: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/6C.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1310	100.0	585	US-08-937-067-9	Sequence 9, Appl
2	823.5	62.9	685	US-08-937-067-14	Sequence 14, Appl
3	477	36.4	565	US-08-937-067-8	Sequence 8, Appl
4	440.5	33.6	572	US-08-937-067-13	Sequence 13, Appl
5	372	28.4	325	US-08-878-474-9	Sequence 9, Appl
6	367	28.0	323	US-08-878-474-7	Sequence 7, Appl
7	360	27.5	318	US-08-878-474-3	Sequence 3, Appl
8	304.5	23.2	666	US-08-937-067-10	Sequence 10, Appl
9	289.5	22.9	537	US-08-937-067-11	Sequence 11, Appl
10	282	21.5	706	US-08-967-289-2	Sequence 2, Appl
11	278.5	21.3	295	US-08-937-067-2	Sequence 12, Appl
12	271	20.7	709	US-08-937-067-12	Sequence 4, Appl
13	270	20.6	212	US-08-937-067-4	Sequence 6, Appl
14	270	20.6	317	US-08-937-067-6	Sequence 6, Appl
15	244.5	18.7	295	US-08-893-654B-6	Sequence 2, Appl
16	234	17.9	314	US-08-937-067-7	Sequence 4, Appl
17	231.5	17.7	281	US-08-893-654B-2	Sequence 2, Appl
18	229	17.5	280	US-08-893-654B-4	Sequence 4, Appl
19	180.5	13.8	641	US-09-233-989-10	Sequence 10, Appl
20	139.5	10.6	787	US-08-720-484A-4	Sequence 4, Appl
21	139.5	10.6	787	US-08-953-823A-4	Sequence 4, Appl
22	139.5	10.6	787	US-08-358-239-4	Sequence 4, Appl
23	130	9.9	793	US-08-720-484A-2	Sequence 2, Appl
24	130	9.9	793	US-08-953-823A-2	Sequence 2, Appl
25	130	9.9	793	US-09-293-505-16	Sequence 16, Appl
26	130	9.9	793	US-09-293-505-17	Sequence 17, Appl
27	130	9.9	793	US-09-398-239-2	Sequence 2, Appl

28	130	9.9	803	US-09-293-505-15	Sequence 15, Appl
29	97.5	7.4	1461	US-09-585-887-9	Sequence 9, Appl
30	97.5	7.4	1461	US-09-289-578-9	Sequence 9, Appl
31	95.5	7.3	265	US-08-918-288-39	Sequence 39, Appl
32	95.5	7.3	265	US-09-282-357-39	Sequence 39, Appl
33	95	7.3	265	US-08-918-288-3	Sequence 3, Appl
34	95	7.3	265	US-09-282-357-3	Sequence 3, Appl
35	94.5	7.2	869	US-08-644-271-29	Sequence 16, Appl
36	94.5	7.2	869	US-08-479-233-11	Sequence 11, Appl
37	94.5	7.2	869	US-09-077-955-33	Sequence 33, Appl
38	93.5	7.1	585	US-09-930-181-17	Sequence 4, Appl
39	93.5	7.1	603	US-09-930-181-1	Sequence 1, Appl
40	93.5	7.1	668	US-09-930-181-2	Sequence 2, Appl
41	92	7.0	160	US-08-479-233-11	Sequence 11, Appl
42	92	7.0	160	PCT-US93-00643-11	Sequence 11, Appl
43	92	7.0	902	US-08-196-479B-6	Sequence 6, Appl
44	92	7.0	902	US-08-818-823-6	Sequence 6, Appl
45	90	6.9	868	PCT-US95-08493-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-937-067-9
Sequence 9, Application US/08937067
Patent No. 6433155
GENERAL INFORMATION:
APPLICANT: Umanaky, Samuil
APPLICANT: Melkonyan, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SBO ID NO.: 9.7
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-937-067-9
Query Match 100.0%; Score 1310; DB 4; Length 585;
Best Local Similarity 100.0%; Pred. No. 3.9e-115;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARPPSPAPSLLLLLLAQLVGRRAAASKAPVCCETVPMCRGIGYVLTMPNPFNHDQ 60
DB 1 MARPPSPAPSLLLLLLAQLVGRRAAASKAPVCCETVPMCRGIGYVLTMPNPFNHDQ 60

Qy 61 DEAGLEVHQMFLVLEIQCSDDLRFLLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPLM 120
 Db 61 DEAGLEVHQMFLVLEIQCSDDLRFLLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPLM 120
 Qy 121 ROYGFAMPERMSCDRLPVIGRDAEVLICMDYNSEATAPPPRPAPKPTLPGGPGAPASGG 180
 Db 121 ROYGFAMPERMSCDRLPVIGRDAEVLICMDYNSEATAPPPRPAPKPTLPGGPGAPASGG 180
 Qy 181 ECPAGGPFVCKREPFVPLIKESHPLYNKRVGTGVPNCVAPCCOSFSADERTFA 235
 Db 181 ECPAGGPFVCKREPFVPLIKESHPLYNKRVGTGVPNCVAPCCOSFSADERTFA 235

RESULT 2

US-08-937-067-14
 ; Sequence 14, Application US/08937067
 ; Patent No. 6433155

GENERAL INFORMATION:

APPLICANT: Umansky, Samuil

APPLICANT: Melkonyan, Hovsep

TITLE OF INVENTION: A FAMILY OF GENES ENCODING

TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,067

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 685 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-937-067-14

Query Match 62.9%; Score 823.5; DB 4; Length 685;
 Best Local Similarity 60.0%; Pred. No. 2.4e-69;
 Matches 159; Conservative 24; Mismatches 39; Indels 43; Gaps 8;

Qy 11 SLT--LLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNTLTMNQFNHDTODEAGLEVH 68
 Db 11 SLTAAVLAVGRSSGAASAKELACQETIVPLCKGIGYNTYTMNQFNHDTODEAGLEVH 70
 Qy 69 QFWPLVLEIQCSDDLRFLLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPLMROYGFAMP 128
 Db 71 QFWPLVLEIQCSDDLRFLLCTMYTPICLPDYHKPLPPCRSVCERAKAGCAPLMROYGFAMP 130
 Qy 129 ERMSCDRLPVIGRDAEVLICMDYNSEATAPPPRPAPKPTLPGGPGAPASGG 174
 Db 131 DMRCDRLPEQG-NPDYLCMDYNRTDLTTAADSPPRRLPPPP-PGEOPPSGSGHSRPPG 188

Qy 175 A-----PAGSGEC--PAGGPFV-----CKREPFVPLIKESHPLYNK 209
 Db 189 ARPRHGGSSSGSGDAAPPSRGCKARPPGGAAPCEGQCRAPMVSVSEHRPLYNR 248
 Qy 210 VRTGVNCAVPCICPSPFSADERTF 234
 Db 249 VKTGOIANCALPCNHPFSODERAF 273

RESULT 3

US-08-937-067-8
 ; Sequence 8, Application US/08937067
 ; Patent No. 6433155

GENERAL INFORMATION:

APPLICANT: Umansky, Samuil

APPLICANT: Melkonyan, Hovsep

TITLE OF INVENTION: A FAMILY OF GENES ENCODING

TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,067

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 565 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-937-067-8

Query Match 36.4%; Score 477; DB 4; Length 565;
 Best Local Similarity 41.9%; Pred. No. 6.7e-37;
 Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;

Qy 3 RPDSSAPPSLLLLAQLVGRRAAASKAPV-----COEITVPMCRGIGYNTLTMNQF 55
 Db 2 RPRSAFLPLPLLLPAAGPAQPHGKGISIPHGFCQPSITLCTDIAVNMQIMPL 61
 Qy 56 NHDQDEAGLEVHQMFLVLEIQCSDDLRFLLCTMYTPICLPDYHKPLPPCRSVCERAKAG 115
 Db 62 GHTNQDEAGLEVHQMFLVLEIQCSDDLRFLLCTMYTPICLPDYHKPLPPCRSVCERAKAG 120
 Qy 116 CSPLMROYGFAMPBERMSCDRLPVIGRDAEVLICMDYNSE-----ATTAPRPAPA-KPT 168
 Db 121 CEALMNKKGFPWPERLRKEHPRRG--AEQICVQGNHSEDPALTLTAP--PGIQPG 175
 Qy 169 LRGPPGAPASGECPPAGS-----PFVCKCRPEFVPLIKESHPLYNKRVGTGVPNCVAPCYQ 224
 Db 176 AGTIPGGGGGGGAPPRATVLEHPHCP-----RVLKV--PSYLSYKFLGGRDCAAPC-E 226
 Qy 225 PS-----FSADERTFA 235

Db 227 PARPDGSMFSGQETRPA 244

RESULT 4

US-08-937-067-13
Sequence 13, Application US/08937067
Patent No. 643315
GENERAL INFORMATION:
APPLICANT: Umanaky, Samuel
APPLICANT: Melkonian, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 572 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-937-067-13

Query Match 33.6%; Score 440.5; DB 4; Length 572;
Best Local Similarity 38.8%; Pred. No. 1.8e-33;
Matches 100; Conservative 36; Mismatches 75; Indels 47; Gaps 12;

QY 8 APPSLLLLLAQLVGRRAAASKAP-----VCOEITVPMCRGIGYNLTMPN 53
Db 11 SPLGICALVLA-LGALPTDTRAOYHGEKISVDFHFCOPISTPLTDIAHNOTIIPN 69
QY 54 QFNHTDDEAGLEVHQPVLVEIQSPDLRFELCTMYTPICLPDYHKBPLPCRSVCERAK 113
Db 70 LLGHTNODAGLEVHQPVLVAVKQSPDLRFELCSMVAIPVCTV-LDQAIPCRSICERAR 128
QY 114 AGCSPLMROVGFAMPERMSCRLPLVGRDAVLCMDYKRSERT--TAPPPFPKAPLPLP 170
Db 129 QGCEALMKNKFFQWPERLRCENFPVHG--AGEICVQNTSGSGAGSPYAPYAPLPLP 186
QY 171 GPSPAPASGSGECPAGG-----PFVCKCREPFPVLKESHPLYNKRTGOVNCAPCYO 224
Db 187 DPFTAMS-----PSDGRRLSFPSCP-RQLKVP-----PYLGTRFLGE-RDCGAPC-E 233
QY 225 PS-----PSADERTPA 235
Db 234 PGRANGLMYFKEERRFA 251

RESULT 5

US-08-878-474-9
Sequence 9, Application US/08878474
Patent No. 6133232
GENERAL INFORMATION:
APPLICANT: De Robertis, Edward M.
APPLICANT: Boumeester, Lewis
TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
TITLE OF INVENTION: Factors
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hase
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,474
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,150
FILING DATE: 20-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 3100.002US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/248-5500
TELEFAX: 415/362-5418
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-878-474-9

Query Match 28.4%; Score 372; DB 4; Length 325;
Best Local Similarity 35.6%; Pred. No. 2.5e-27;
Matches 80; Conservative 34; Mismatches 81; Indels 30; Gaps 7;

QY 10 PSLILLLLAQLVGRRA-----AASKAPVCOEITVPMCRGIGYNLTMPN 63
Db 6 PGMLLRAGLLAALCLLRVPGARAACEPVRIPLCKSLPMNMTKMPNHLHSTQANA 65
QY 64 GLEHOFMPVLVEIQSPDLRFELCTMYTPICLPDY-HKPLPRCSVGERAKGSPMLRQ 122
Db 66 ILAIEQEGELGTHCSPLDLFFLCAMTAPICTIDFQHEPIPCSVGERAQGEPLIK 125
QY 123 YGFAMPERMSCDLPLVGRDAVLCMDYNSSEATTAPPPFPKAPLPLPGRGAPASGEC 182
Db 126 YRSHMPENLACEELPYVDRG---VCI--SPRAYTAAGADFP-----MSSNQC 170
QY 183 PAGSPFVCKCREPFPVLKESHPL-----YNNKRTGOVNCAPCY 223
Db 171 RGASSERCKK---PIRATQKTYFRNNYVIRAKVKEIKTKCH 211

RESULT 6

US-08-878-474-7
Sequence 7, Application US/08878474
Patent No. 6133232
GENERAL INFORMATION:
APPLICANT: Boumeester, Lewis
APPLICANT: De Robertis, Edward M.
TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
TITLE OF INVENTION: Factors

```

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Majestic, Parsons, Siebert & Hsue
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,474
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,150
FILING DATE: 20-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 3100.002US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/362-5418
TELEFAX: 415/362-5418
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-878-474-7

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Query Match      28.0%; Score 367; DB 4; Length 323;
Best Local Similarity 35.8%; Pred. No. 7.3e-27;
Matches 77; Conservative 34; Mismatches 80; Indels 24; Gaps 6;

QY 14 LLLLAQLVGRRAAASKAPVCOEITVPMCGIGYNTLHMENQFNHDTODAGLEVHGFML 73
DB 16 LLLLAQLVGRRAAASKAPVCOEITVPMCGIGYNTLHMENQFNHDTODAGLEVHGFML 75
QY 74 VEIQSPDLRFELCTMYTPTICLPDY-HKPLPGRSVYCEERAKAGCSPLMROYGFAWERM 132
DB 76 LETHCSDDLFLFCAMVAICTIDFQHEPIKPKSVCEERARQCEIILIKYHNSWESLA 135
QY 133 CRLPYLGDAVLCMDVNRSEATTAPRRPFAKPTLPGPPGAPASGEGCPAGGPFVCKC 192
DB 136 CDELFPYDGG---VCI--SPEAIVTADGADFP-----MDSSTGHCRCGASSEKCKC 180
QY 193 REPFPVILKESHPL-----YNNKRTGQVPCAVPCY 223
DB 181 K---FVRATQKTYFRNNYIVIRAKVKVKYKCH 211

```

```

RESULT 7
US-08-878-474-3
Sequence 3, Application US/08878474
Patent No. 6133232
GENERAL INFORMATION:
APPLICANT: De Robertis, Edward M.
APPLICANT: Boumeester, Lewis
TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
TITLE OF INVENTION: Factors
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Majestic, Parsons, Siebert & Hsue
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94111-4106

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,474
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,150
FILING DATE: 20-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 3100.002US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/248-5500
TELEFAX: 415/362-5418
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-878-474-3

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```

Query Match      27.5%; Score 360; DB 4; Length 318;
Best Local Similarity 37.1%; Pred. No. 3.2e-26;
Matches 83; Conservative 34; Mismatches 73; Indels 34; Gaps 10;

QY 8 APPSLLLLLAQLVGRRAAASKAPVCOEITVPMCGIGYNTLHMENQFNHDTODAGLEV 67
DB 14 AIPGLALLLP---NAVCAS---CEPVRIIPMCKSMWNMTKMNHLHSTQANAILAI 65
QY 68 HOFWFLVEIQSPDLRFELCTMYTPTICLPDY-HKPLPGRSVYCEERAKAGCSPLMROYGFA 126
DB 66 EGFEGILLTTECSQDILFLFCAMVAICTIDFQHEPIKPKSVCEERARQCEIILIKYHNT 125
QY 127 WERNSCRLPYLGDAVLCMDVNRSEATTAPRRPFAKPTLPGPPGAPASGEGCPAGG 186
DB 126 WESLACEELFPYDGG---VCIS---PEAIVTVEQGTSMDF-----SMDSNNGCGSGR 175
QY 187 PFVCKCREPFVPI-----LKESHPLYNKRTGQVPCAVPCY 223
DB 176 EH-CKCK---PMKATQKTYLKN---YNYVIRAKVKVKYKCH 211

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RESULT 8
US-08-937-067-10
Sequence 10, Application US/08937067
Patent No. 6433155
GENERAL INFORMATION:
APPLICANT: Umanaky, Samuil
APPLICANT: Melkonyan, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067

```

FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 666 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-937-067-10

Query Match 23.2%; Score 304.5; DB 4; Length 666;
Best Local Similarity 34.5%; Pred. No. 1.3e-20;
Matches 80; Conservative 27; Mismatches 76; Indels 49; Gaps 10;

QY 12 LLLLLLQVGRRAAASAPVCOEITVPMCRGIGYNTLTHMPNQFNHDTODEAGLEVHOFW 71
DB 12 LTVFLQIGHSLSFS-----CEPITLMCODLPYNTTFMNLNHYDQOTPALAMEBFH 66
QY 72 PLVEICSPDLRFICTMYTPICLPDYHKPLPPCRSVCEKAKGCSPLMRQYGFAMPERM 131
DB 67 PMVUDCSRDRPPLCALYAPICM-EYGRVTLPCRRLCQRAYSECSKLMENFGVPMPEDM 125
QY 132 SCDBLPVLRDAEVLCDMDYNSEATTAAPRPFPAPKPTLPGPP--GAPAS-----GGECPA 184
DB 126 ECSRFP-----DCD-----EPYRLVDNLVGDPTGAPVAVQORDGFWCP- 166
QY 185 GGPVCKCRFPVFLKESHP-LYNKATGQYPCNAVCYCPSSADRTTA 235
DB 167 -----RE-----LKIDPLGYSFL--HVRDCSPCPMYPFRELSPA 202

RESULT 9
US-08-937-067-11
Sequence 11, Application US/08937067
Patent No. 6433155
GENERAL INFORMATION:
APPLICANT: Umansky, Samuil
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 537 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-937-067-11

Query Match 22.9%; Score 299.5; DB 4; Length 537;
Best Local Similarity 34.1%; Pred. No. 3e-20;
Matches 59; Conservative 32; Mismatches 67; Indels 15; Gaps 4;

QY 14 LLLLAQVGRRAAASAPVCOEITVPMCRGIGYNTLTHMPNQFNHDTODEAGLEVHOFWPL 73
DB 28 LLLRLPLGDEDEER--CDPIRIAMCQNLGVVTKMPNLVGHLEQTDALQLTTFTPL 85
QY 74 VEIQCSPDLRFICTMYTPICLPDYHKPLPPCRSVCEKAKGCSPLMRQYGFAMPERMSC 133
DB 86 IYQCSQLOFFLCISYVPMCTEKINIPICGCGMCLSVKRCSPVLRFGFAMPDTLNC 145
QY 134 DRPLVLRDAEVLCDMDYNSEATTAAPRPFPAPKPTLPGPPAPASGGECPAGC 186
DB 146 SKRPP-QNDHNMCMGEGDEEVLPHKT-PIQP-----GGECHSVG 185

RESULT 10
US-08-987-289-2
Sequence 2, Application US/08987289
Patent No. 5994098
GENERAL INFORMATION:
APPLICANT: HU, ERDING
TITLE OF INVENTION: A Human 7-TM Receptor Similar
TITLE OF INVENTION: to Murine Fizzled-6 gene
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,289
FILING DATE: 09-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,725
FILING DATE: 02-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70060
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 706 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-987-289-2
Query Match 21.5%; Score 282; DB 2; Length 706;

Best Local Similarity 30.8%; Pred. No. 1.8e-18;
Matches 65; Conservative 22; Mismatches 80; Indels 44; Gaps 6;
QY 33 COEIVPCRGVGNLTMPNOFNHDTODEAGLEVHGFVPLVEIOSPDRLFTMTPT 92
Db 24 CEPVPCRMKAYMTFFPNLMGHYDOSIAVEMHFLPLNTEFCSPITEFLCKAFV 83
QY 93 ICLPDYHKPLPEPCRSVCERAKAGCSPLMRQYGFAMPBERMSCDRLPVLGRDAEVLCDYNR 152
Db 84 TCIEGDIH-VVPECRKLCERKVS DCKLIDTFGI RMPELECRQLQYCEBTVV----- 135
QY 153 SEATTAAPRRPF--PAKPTLPGPBGAPASGGECPAGGPFVCKCRBPVPLKESHPLYNKV 210
Db 136 ---TFDPHTEFGPOKET-----EQYORDIGFWC-----PRHLKT 167
QY 211 RTGQ-----VNCAPVCQPSFSADERTFA 235
Db 168 SGGGGRKFLGIDQCAPPCPMYFKSDELEFA 198

RESULT 11

US-08-937-067-2

Sequence 2, Application US/08937067

Patent No. 6433155

GENERAL INFORMATION:

APPLICANT: Umansky, Samuil

APPLICANT: Melkonyan, Hovsep

TITLE OF INVENTION: A FAMILY OF GENES ENCODING

TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND

TITLE OF INVENTION: METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,067

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 295 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-937-067-2

Query Match 21.3%; Score 278.5; DB 4; Length 295;
Best Local Similarity 36.2%; Pred. No. 1.3e-18;
Matches 63; Conservative 27; Mismatches 61; Indels 23; Gaps 7;

QY 6 PSAPSLILLIAQ-----LVGRAAASAPVCOEI--TVPCRGIGYNLTMP 52

Db 2 PRGPAISLLLVASHCISAGLFLFGOPDRSYKTNCKPIPAVLQCHGIEYQNMRLP 61

QY 53 NQFNHDTODEAGLEVHGFVPLVEIOSPDRLFTMTPTCLPDYHKPLPEPCRSVCER 111

Db 62 NLGHEITMKEY-LEQAGAMITLVMKQCHPDTKFLCSLFAVCLDDLDDETIQPCSLCVQ 120

QY 112 AKAGCSPLMRQYGFAMPBERMSCDRLPVLGRDAEVLCDYNRSE----ATTAPR 161
Db 121 VKDCAPFMSAFGPWPDMLECDRPF---QDND-LCLPLASSDHLDPATEBAPK 170

RESULT 12

US-08-937-067-12

Sequence 12, Application US/08937067

Patent No. 6433155

GENERAL INFORMATION:

APPLICANT: Umansky, Samuil

APPLICANT: Melkonyan, Hovsep

TITLE OF INVENTION: A FAMILY OF GENES ENCODING

TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND

TITLE OF INVENTION: METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,067

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 709 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-937-067-12

Query Match 20.7%; Score 271; DB 4; Length 709;
Best Local Similarity 30.6%; Pred. No. 2e-17;
Matches 71; Conservative 22; Mismatches 95; Indels 44; Gaps 8;

QY 10 PSLLILLIAQLVGRAAASAPVCOEITVPCRGIGYNLTMPNOFNHDTODEAGLEVH 69

Db 5 PFLACILPLV---RGHSIFTECEPITVPCRMKMTVMNTFFPNLMGHYDOSIAVEMH 60

QY 70 FWPVLEIOGSPDLRFPLCTMTPTCLPDYHKPLPEPCRSVCERAKAGCSPLMRQYGFAMP 129

Db 61 FLHLANLSCSPNIMFICQAPITPTCTQIHVL--PCKRLCEKIVSDCKLMDTFGIHMP 119

QY 130 RMSCDRLPVLGRDAEVLCDYNRSEATTAPRPPPAKPTLPGPBGAPASGGECPAGGPFV 189

Db 120 ELECNRLP-----HCDD-----TVPVTSHP-HTELSGF---QKSDQVPRDIGFW 160

QY 190 CKCREPVPVPLIKESHPLYNKYRTGQ-----VNCAPVCQPSFSADERTFA 235

Db 161 C-----PKHLRTSGDQGYRFLGIEQCAPPCPMYFKSDELDLFA 198

RESULT 13

US-08-937-067-4

Sequence 4, Application US/08937067

```

; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Umaneky, Samuel
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-937-067-4

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Query Match 20.6%; Score 270; DB 4; Length 212;

Best Local Similarity 31.3%; Pred. No. 5.6e-18; Matches 73; Conservative 27; Mismatches 81; Indels 52; Gaps 10;

```

Qy 9 PPSLLLLLAQ-----LVGRAAASAKAVCOEI--TVMCRGIGYNLTHMPNQF 55
Db 5 PPSLLFLFASHCCLGSRGLFLFGQPDFSYKSNCKRIPANLQCHIEIQNNRLPLL 64
Qy 56 NHTQDEAGLEVHOFM-PLVEIQCSPLIRFPLCTMYTPICLPDYHKKPLPRCSVCERAKA 114
Db 65 GHETMKREV-LEQAGAWIPLVKQCHPDKFKLCSLFAVCLDDIDETIQCHSXCVQVKD 123
Qy 115 GCSPLMROYGFWPBERMSCDLPLVGRDAEVLCDYNSEKATTPRRFPKPLPGPFG 174
Db 124 RCAVWMAFGFWPMDMECDRFP--QDND-LCTPLASSD-----HLLPATEE 167
Qy 175 APASGEGCPAGPFVCK-----CREPFVPLIKESHPLVYNKVTGQ 214
Db 168 APK---VCEA-----CKNKDNDNDIMETLCKNDPALKIKYKEITYINRRGR 212

```

RESULT 14
US-08-937-067-6

; Sequence 6, Application US/08937067

; Patent No. 6433155

; GENERAL INFORMATION:

; APPLICANT: Umaneky, Samuel

; APPLICANT: Melkonian, Hovsep

; TITLE OF INVENTION: A FAMILY OF GENES ENCODING

; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND

; TITLE OF INVENTION: METHODS OF USE THEREOF

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: MORRISON & FOERSTER

```

; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-937-067-6

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Query Match 20.6%; Score 270; DB 4; Length 317;

Best Local Similarity 38.2%; Pred. No. 9.2e-18; Matches 52; Conservative 24; Mismatches 50; Indels 10; Gaps 5;

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Qy 28 SKAVCOEI--TVMCRGIGYNLTHMPNQFNHODAGLEVHOFVLEIQCSPLIRF 85
Db 48 SKPQCIDPADLPCTVGVKRNRLPNLLEHSLAEVKKQASSWPLAKRCHSDTQVF 107
Qy 86 LCTWYTPICLPDYHKKPLPRCSVCERAKACSPLMROYGFWPBERMSCDLPLVGRDAEV 145
Db 108 LCSLFAVCL---DRPIYPRCSLCEAVRACAPLMEAYGFWPBERMLHCHKFP-LDND--- 160
Qy 146 LCMQDYNSE-ATTAP 160
Db 161 LCTAVQFGLPATAP 176

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RESULT 15

US-08-937-654B-6

; Sequence 6, Application US/08893654B

; Patent No. 6165748

; GENERAL INFORMATION:

; APPLICANT: RACIE, LISA, ET ALIA

; TITLE OF INVENTION: Frazzled NUCLEOTIDE SEQUENCES,

; TITLE OF INVENTION: EXPRESSION PRODUCTS, COMPOSITIONS AND USES

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: GENETICS INSTITUTE, INC.

; STREET: 87 CAMBRIDGE PARK DRIVE

; CITY: CAMBRIDGE

; STATE: MA

; COUNTRY: USA

; ZIP: 02140-2387

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/893,654B

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: MEINERT, M.C.

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 19, 2003, 16:35:02 ; Search time 22 Seconds
(without alignments)
1030.270 Million cell updates/sec

Title: US-09-847-102a-68
Perfect score: 1310
Sequence: 1 MARPPSAPPSLLLLLAQL.....PNCAPVCPQPSFSADERTFA 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

Total number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB pep.*
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6: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB pep.*
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8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB pep.*
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10: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB pep.*
11: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB pep.*
12: /cgn2_6/prodata/2/pubpaa/US10_PUBCOMB pep.*
13: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1310	100.0	235	US-09-847-102a-68	Sequence 68, App1
2	1310	100.0	585	US-10-146-474-9	Sequence 9, App1
3	1310	100.0	585	US-09-847-102a-51	Sequence 51, App1
4	1310	100.0	586	US-10-152-548-10	Sequence 10, App1
5	1111	84.8	516	US-09-847-102a-38	Sequence 38, App1
6	824	62.9	277	US-09-847-102a-73	Sequence 73, App1
7	824	62.9	694	US-09-847-102a-56	Sequence 56, App1
8	823.5	62.9	274	US-09-847-102a-74	Sequence 74, App1
9	823.5	62.9	682	US-10-152-548-16	Sequence 16, App1
10	823.5	62.9	685	US-10-146-474-14	Sequence 14, App1
11	823.5	62.9	685	US-09-847-102a-57	Sequence 57, App1
12	740.5	56.5	599	US-09-847-102a-37	Sequence 37, App1
13	621	47.4	694	US-10-152-548-2	Sequence 2, App1
14	585	44.7	570	US-09-847-102a-43	Sequence 43, App1
15	477	36.4	244	US-09-847-102a-63	Sequence 63, App1
16	477	36.4	565	US-10-146-474-8	Sequence 8, App1
17	477	36.4	565	US-09-847-102a-46	Sequence 46, App1
18	461	35.2	253	US-09-847-102a-71	Sequence 71, App1
19	461	35.2	574	US-09-847-102a-54	Sequence 54, App1

20	440.5	33.6	251	9	US-09-847-102a-72	Sequence 72, App1
21	440.5	33.6	572	9	US-10-146-474-13	Sequence 13, App1
22	440.5	33.6	572	9	US-09-847-102a-55	Sequence 55, App1
23	440.5	33.6	573	9	US-10-152-548-14	Sequence 14, App1
24	424	32.4	529	9	US-09-847-102a-41	Sequence 41, App1
25	422	32.2	314	9	US-09-847-102a-62	Sequence 62, App1
26	422	32.2	626	9	US-09-847-102a-45	Sequence 45, App1
27	415	31.7	319	9	US-09-847-102a-61	Sequence 61, App1
28	415	31.7	647	9	US-09-847-102a-75	Sequence 75, App1
29	394.5	30.1	231	9	US-09-847-102a-75	Sequence 76, App1
30	394.5	30.1	232	9	US-09-847-102a-58	Sequence 58, App1
31	394.5	30.1	591	9	US-09-847-102a-59	Sequence 59, App1
32	384	29.3	227	9	US-09-847-102a-77	Sequence 77, App1
33	384	29.3	581	9	US-09-847-102a-60	Sequence 60, App1
34	380.5	29.0	533	9	US-09-847-102a-39	Sequence 39, App1
35	378	28.9	544	9	US-09-847-102a-40	Sequence 40, App1
36	372	28.4	325	9	US-09-803-170C-9	Sequence 9, App1
37	372	28.4	325	9	US-09-974-298-17	Sequence 17, App1
38	372	28.4	325	9	US-10-090-049-4	Sequence 4, App1
39	372	28.4	325	10	US-09-903-187A-9	Sequence 9, App1
40	372	28.4	325	10	US-09-903-187A-9	Sequence 9, App1
41	372	28.4	325	10	US-09-903-171A-9	Sequence 9, App1
42	372	28.4	325	10	US-09-903-188A-9	Sequence 9, App1
43	372	28.4	325	10	US-09-903-323A-9	Sequence 9, App1
44	372	28.4	325	10	US-09-903-323A-9	Sequence 9, App1
45	372	28.4	325	10	US-09-903-323A-9	Sequence 9, App1

ALIGNMENTS

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RESULT 1
US-09-847-102a-68
; Sequence 68, Application US/09847102A
; Publication NO. US20030044409A1
; GENERAL INFORMATION:
; APPLICANT: University of California
; APPLICANT: Carson, Dennis A.
; APPLICANT: Corr, Maripac
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Lorenzo, Leon M.
; APPLICANT: Malini, Sen
; TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
; STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
; FILE REFERENCE: 22000-20629.00
; CURRENT APPLICATION NUMBER: US/09/847,102A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-102a-68

Query Match      100.0%  Score 1310; DB 9; Length 235;
Best Local Similarity 100.0%  Pred. No. 1e-97;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPPSAPPSLLLLLAQLVGRRAAASKAPVCOEITVPCRCRIGVNLTHMPQFNHDTQ 60
Db 1 MARPPSAPPSLLLLLAQLVGRRAAASKAPVCOEITVPCRCRIGVNLTHMPQFNHDTQ 60
QY 61 DEAGLEVHQWPLVEIQCSFDLRFPLCTMYTPICLDYHNPPLPCCSVCRRAAGCSPLM 120
Db 61 DEAGLEVHQWPLVEIQCSFDLRFPLCTMYTPICLDYHNPPLPCCSVCRRAAGCSPLM 120
QY 121 ROYGFAMPEMSSCDRLPVLCGRDAEVLICMDYRSEATTAAPPAPPAKPTLPGPAPASGG 180
Db 121 ROYGFAMPEMSSCDRLPVLCGRDAEVLICMDYRSEATTAAPPAPPAKPTLPGPAPASGG 180
QY 181 ECPAGGFVCKEPPVPIIKESHPLYNKVRTGQVNCAPVCYQPSFSADERTFA 235
Db 181 ECPAGGFVCKEPPVPIIKESHPLYNKVRTGQVNCAPVCYQPSFSADERTFA 235
```

Db 181 ECPAGGFVCKREPFVILKESHPLYNKVRTGQVNCVPCYQPSFSADERTFA 235

RESULT 2

US-10-146-474-9
Sequence 9, Application US/10146474
Publication No. US20030023061A1
GENERAL INFORMATION:
APPLICANT: Umaneky, Samu'l
Melkonyan, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & ROEBSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,474
FILING DATE: 14-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-146-474-9

Query Match 100.0%; Score 1310; DB 9; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.7e-97;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPPSAPSLILLILLAQLVGRRAAASKAPVCOEITVPMCRGIGYVLTMPNQFNHDTQ 60
Db 1 MARPPSAPSLILLILLAQLVGRRAAASKAPVCOEITVPMCRGIGYVLTMPNQFNHDTQ 60
QY 61 DEAGLEVHQFVPLVEIQCSDDLRFLLCTMTYPTICLPDYHKPLPPCRSVCCERAKGCSPLM 120
Db 61 DEAGLEVHQFVPLVEIQCSDDLRFLLCTMTYPTICLPDYHKPLPPCRSVCCERAKGCSPLM 120
QY 121 ROYGFAMPERMSCDRLPVLRGDAEVLCDYNRSEATTAPPRFPKPTLPGPFGAPASGG 180
Db 121 ROYGFAMPERMSCDRLPVLRGDAEVLCDYNRSEATTAPPRFPKPTLPGPFGAPASGG 180
QY 181 ECPAGGFVCKREPFVILKESHPLYNKVRTGQVNCVPCYQPSFSADERTFA 235
Db 181 ECPAGGFVCKREPFVILKESHPLYNKVRTGQVNCVPCYQPSFSADERTFA 235

RESULT 3
US-09-847-102A-51

Sequence 51, Application US/09847102A
Publication No. US20030044409A1
GENERAL INFORMATION:
APPLICANT: University of California
APPLICANT: Carson, Dennis A.
APPLICANT: Corr, Maripac
APPLICANT: Rhee, Chae-Seo
APPLICANT: Lorenzo, Leonil M.
APPLICANT: Malini, Sen
TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
FILE REFERENCE: 22000-20629.00
CURRENT APPLICATION NUMBER: US/09/847,102A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: FastSeq. for Windows Version 4.0
SEQ ID NO 51
LENGTH: 585
TYPE: PRT
ORGANISM: Homo sapiens
US-09-847-102A-51

Query Match 100.0%; Score 1310; DB 9; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.7e-97;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPPSAPSLILLILLAQLVGRRAAASKAPVCOEITVPMCRGIGYVLTMPNQFNHDTQ 60
Db 1 MARPPSAPSLILLILLAQLVGRRAAASKAPVCOEITVPMCRGIGYVLTMPNQFNHDTQ 60
QY 61 DEAGLEVHQFVPLVEIQCSDDLRFLLCTMTYPTICLPDYHKPLPPCRSVCCERAKGCSPLM 120
Db 61 DEAGLEVHQFVPLVEIQCSDDLRFLLCTMTYPTICLPDYHKPLPPCRSVCCERAKGCSPLM 120
QY 121 ROYGFAMPERMSCDRLPVLRGDAEVLCDYNRSEATTAPPRFPKPTLPGPFGAPASGG 180
Db 121 ROYGFAMPERMSCDRLPVLRGDAEVLCDYNRSEATTAPPRFPKPTLPGPFGAPASGG 180
QY 181 ECPAGGFVCKREPFVILKESHPLYNKVRTGQVNCVPCYQPSFSADERTFA 235
Db 181 ECPAGGFVCKREPFVILKESHPLYNKVRTGQVNCVPCYQPSFSADERTFA 235

RESULT 4
US-10-152-548-10
Sequence 10, Application US/10152548
Publication No. US20030040051A1
GENERAL INFORMATION:
APPLICANT: Bhanot, Purnima
Brink, Marcel
Harryman, Cindy S.
Wang, Yanahu
Hsieh, Jen-chih
Andrew, Deborah
Nathan, Jeremy
Nusse, Roel

TITLE OF INVENTION: Wnt Receptor Compositions and Methods
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/152,548
FILING DATE: 21-May-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,340
FILING DATE: 11-APR-1997
APPLICATION NUMBER: US 60/015,307
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0167.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 586 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Hf55 protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-152-548-10

Query Match 100.0%; Score 1310; DB 9; Length 586;
Best Local Similarity 100.0%; Pred. No. 2,7e-97;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARDPSAPSLLLLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTMPNPFNDTQ 60
DB 1 MARDPSAPSLLLLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTMPNPFNDTQ 60
QY 61 DEAGLEVHQFWPLVEIQCSDDLRFLLCTMTPTICLPDYHKLPPCRSVCEBAKAGCSPLM 120
DB 61 DEAGLEVHQFWPLVEIQCSDDLRFLLCTMTPTICLPDYHKLPPCRSVCEBAKAGCSPLM 120
QY 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPPPPAKPTLPGPAPASGG 180
DB 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPPPPAKPTLPGPAPASGG 180
QY 181 ECPAGGFVCKREPFVILKESHPLYNKRTGOVNCAPVCYOPFSADERTFA 235
DB 181 ECPAGGFVCKREPFVILKESHPLYNKRTGOVNCAPVCYOPFSADERTFA 235

RESULT 5
US-09-847-102A-38
; Sequence 38, Application US/09847102A
; Publication No. US20030044409A1
; GENERAL INFORMATION:
; APPLICANT: University of California
; APPLICANT: Carson, Dennis A.
; APPLICANT: Corr, Maripat
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Lorenzo, Leoni M.
; APPLICANT: Malini, Sen
; TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
; FILE REFERENCE: 22000-20629.00
; CURRENT APPLICATION NUMBER: US/09/847,102A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-102A-38

Query Match 84.8%; Score 1111; DB 9; Length 516;

Best Local Similarity 87.2%; Pred. No. 2.1e-81;
Matches 205; Conservative 0; Mismatches 0; Indels 30; Gaps 1;
QY 1 MARDPSAPSLLLLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTMPNPFNDTQ 60
DB 1 MARDPSAPSLLLLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTMPNPFNDTQ 60
QY 61 DEAGLEVHQFWPLVEIQCSDDLRFLLCTMTPTICLPDYHKLPPCRSVCEBAKAGCSPLM 120
DB 61 DEAGLEVHQFWPLVEIQCSDDLRFLLCTMTPTICLPDYHKLPPCRSVCEBAKAGCSPLM 120
QY 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPPPPAKPTLPGPAPASGG 180
DB 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPPPPAKPTLPGPAPASGG 180
QY 181 ECPAGGFVCKREPFVILKESHPLYNKRTGOVNCAPVCYOPFSADERTFA 235
DB 181 ECPAGGFVCKREPFVILKESHPLYNKRTGOVNCAPVCYOPFSADERTFA 205

RESULT 6
US-09-847-102A-73
; Sequence 73, Application US/09847102A
; Publication No. US20030044409A1
; GENERAL INFORMATION:
; APPLICANT: University of California
; APPLICANT: Carson, Dennis A.
; APPLICANT: Corr, Maripat
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Lorenzo, Leoni M.
; APPLICANT: Malini, Sen
; TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
; FILE REFERENCE: 22000-20629.00
; CURRENT APPLICATION NUMBER: US/09/847,102A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-102A-73

Query Match 62.9%; Score 824; DB 9; Length 277;
Best Local Similarity 59.9%; Pred. No. 1.1e-58;
Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;

QY 11 SLT--LLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTMPNPFNDTQDEAGLEVH 68
DB 11 SLTAAALLLGRSSGAASAKELACQETITVPLCKIGIYNTVMPNPFNDTQDEAGLEVH 70
QY 69 QFWPLVEIQCSDDLRFLLCTMTPTICLPDYHKLPPCRSVCEBAKAGCSPLMROYGFAWP 128
DB 71 QFWPLVEIQCSDDLRFLLCTMTPTICLPDYHKLPPCRSVCEBAKAGCSPLMROYGFAWP 130
QY 129 ERMSCDRLPVLGRDAEVLCDYNRSEATTAPPPPAKPTLPGPAPASGG 174
DB 131 DRMKCDRLPBOG-NPDTLMDYNRSDTLTTAAPPSPRRLPPPP-PGQPPSGSGHRRPG 187
QY 175 A-----PASGG-----ECPAGGFV-----CKREFPVILKESH 205
DB 188 ARPHRRGGGGGGGDAAPAPARAGGGGGGAKRPPGGGAACFPCQCRAPAVSVSSRRH 247
QY 206 LYNKRTGOVNCAPVCYOPFSADERTF 234
DB 248 LYNKRTGOVNCAPVCYOPFSADERTF 276

RESULT 7
US-09-847-102A-56
; Sequence 56, Application US/09847102A
; Publication No. US20030044409A1

```

: GENERAL INFORMATION:
: APPLICANT: University of California
: APPLICANT: Carson, Dennis A.
: APPLICANT: Corr, Maripat
: APPLICANT: Rhee, Chae-Seo
: APPLICANT: Lorenzo, Leonl M.
: APPLICANT: Malinl, Sen
: TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
: TITLE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
: FILE REFERENCE: 22000-20659.00
: CURRENT APPLICATION NUMBER: US/09/847.102A
: CURRENT FILING DATE: 2001-05-01
: NUMBER OF SEQ ID NOS: 138
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 56
: LENGTH: 694
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-847-102A-56

```

ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: M28 protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16;
US-10-152-548-16

Query Match 62.9%; Score 823.5; DB 9; Length 682;
Best Local Similarity 60.0%; Pred. No. 3e-58;
Matches 159; Conservative 24; Mismatches 39; Indels 43; Gaps 8;

11 SLT-LLLLAQLVGRRAAASAPVCOEITVPMCRGIGYNTLHMPNQHDTODEAGLEVH 68
11 SLTAAVLQRSSGAASAASAKELACQEIITVPLCKGIGYNTYTMNQFNHDTODEAGLEVH 70
69 QFWPLVEIQSPDLRFPLCTMTYTPICLPDYHKKPLPCCRVCERAKAGCSPLMRQYGFAMP 128
71 QFWPLVEIQSPDLRFPLCTMTYTPICLPDYHKKPLPCCRVCERAKAGCAPLMRQYGFAMP 130

129 ERMSCDRLPVLRDAEVLCDVYRSEATTA---PRRFPKPTLPG-----PRG 174
131 DRMKCDRLPEQG-NPDTLCMDYNTDITTAAPSPRRLLPPPP-PGEQPPSGSGHSRPPG 188

175 A-----PASGSEC--PAGCPFV---CKREPFVPLIKESHPLYNK 209
189 ARPHRGSSRGSGDAAPPSRGKARPPGGGAAPCEPCQCCTAPMVSVSEKHPLYNR 248

210 VRTGVNCAVPCYQPSFSADERTF 234
249 VKTQIANCALPCHNPFPSQDERAF 273

RESULT 10
US-10-146-474-14
Sequence 14, Application US/10146474
Publication No. US2003023061A1
GENERAL INFORMATION:
APPLICANT: Umanaky, Samuel
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,474
FILING DATE: 14-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 685 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14;
US-10-146-474-14

Query Match 62.9%; Score 823.5; DB 9; Length 685;
Best Local Similarity 60.0%; Pred. No. 3e-58;
Matches 159; Conservative 24; Mismatches 39; Indels 43; Gaps 8;

11 SLT-LLLLAQLVGRRAAASAPVCOEITVPMCRGIGYNTLHMPNQHDTODEAGLEVH 68
11 SLTAAVLQRSSGAASAASAKELACQEIITVPLCKGIGYNTYTMNQFNHDTODEAGLEVH 70
69 QFWPLVEIQSPDLRFPLCTMTYTPICLPDYHKKPLPCCRVCERAKAGCSPLMRQYGFAMP 128
71 QFWPLVEIQSPDLRFPLCTMTYTPICLPDYHKKPLPCCRVCERAKAGCAPLMRQYGFAMP 130

129 ERMSCDRLPVLRDAEVLCDVYRSEATTA---PRRFPKPTLPG-----PRG 174
131 DRMKCDRLPEQG-NPDTLCMDYNTDITTAAPSPRRLLPPPP-PGEQPPSGSGHSRPPG 188

175 A-----PASGSEC--PAGCPFV---CKREPFVPLIKESHPLYNK 209
189 ARPHRGSSRGSGDAAPPSRGKARPPGGGAAPCEPCQCCTAPMVSVSEKHPLYNR 248

210 VRTGVNCAVPCYQPSFSADERTF 234
249 VKTQIANCALPCHNPFPSQDERAF 273

RESULT 11
US-09-847-102a-57
Sequence 57, Application US/09847102A
Publication No. US2003004409A1
GENERAL INFORMATION:
APPLICANT: University of California
APPLICANT: Carson, Dennis A.
APPLICANT: Corr, Maripat
APPLICANT: Rhee, Chae-Seo
APPLICANT: Lorenzo, Leon M.
TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
FILE REFERENCE: 22000-20629.00
CURRENT APPLICATION NUMBER: US/09/847,102A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 57
LENGTH: 685
TYPE: PRT
ORGANISM: Mouse
US-09-847-102a-57

Query Match 62.9%; Score 823.5; DB 9; Length 685;
Best Local Similarity 60.0%; Pred. No. 3e-58;
Matches 159; Conservative 24; Mismatches 39; Indels 43; Gaps 8;

11 SLT-LLLLAQLVGRRAAASAPVCOEITVPMCRGIGYNTLHMPNQHDTODEAGLEVH 68
11 SLTAAVLQRSSGAASAASAKELACQEIITVPLCKGIGYNTYTMNQFNHDTODEAGLEVH 70
69 QFWPLVEIQSPDLRFPLCTMTYTPICLPDYHKKPLPCCRVCERAKAGCSPLMRQYGFAMP 128
71 QFWPLVEIQSPDLRFPLCTMTYTPICLPDYHKKPLPCCRVCERAKAGCAPLMRQYGFAMP 130

129 ERMSCDRLPVLRDAEVLCDVYRSEATTA---PRRFPKPTLPG-----PRG 174
131 DRMKCDRLPEQG-NPDTLCMDYNTDITTAAPSPRRLLPPPP-PGEQPPSGSGHSRPPG 188

175 A-----PASGSEC--PAGCPFV---CKREPFVPLIKESHPLYNK 209
189 ARPHRGSSRGSGDAAPPSRGKARPPGGGAAPCEPCQCCTAPMVSVSEKHPLYNR 248

QY 210 VRTGVPCAVPCYQPSFSDERTF 234
Db 249 VKTGIANCALPCNPFPSQDERAF 273

RESULT 12

US-09-847-102A-37
Sequence 37, Application US/09847102A
Publication No. US20030044409A1
GENERAL INFORMATION:
APPLICANT: University of California
APPLICANT: Carson, Dennis A.
APPLICANT: Cort, Maripat
APPLICANT: Rhee, Chae-Seo
APPLICANT: Lorenzo, Leoni M.
APPLICANT: Malini, Sen
TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
FILE REFERENCE: 22000-20629-00
CURRENT APPLICATION NUMBER: US/09/847,102A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 599
TYPE: PRT
ORGANISM: Mouse
US-09-847-102A-37

Query Match 56.5%; Score 740.5; DB 9; Length 599;
Best Local Similarity 60.3%; Pred. No. 1.2e-51;
Matches 146; Conservative 20; Mismatches 43; Indels 33; Gaps 7;

QY 11 SLL--LILLAQVGRASAKAPVCOEITVPMCRGIGYNTLTHMPQNFHDTODEAGLEVH 68
Db 11 SLLAALAVQRRSGAAASAKELACOEITVPLCKGIGYNTYMPQNFHDTODEAGLEVH 70
QY 69 QFWPLVEIQCSFDLRFPLCTMYTPICLPDYHKPLPPCRSVCCERAKAGCSPLMROYGFAMP 128
Db 71 QFWPLVEIQCSFDLRFPLCTMYTPICLEDYKKPLPPCRSVCCERAKAGCAPLMROYGFAMP 130
QY 129 ERMSCDRLPVLRDAEVLICMDYNRSEATTA--PPRPPAKTLDG-----PPG 174
Db 131 DMRCDRLPEBOG-NPDTLCMDYNRDTLTTAAPSPPRLPPPPP-PGEOPPSGSGHRRPG 188
QY 175 A--PASGGECPAGGFVCKREPPVILKESHPLNKKVRTGVPCAVPCYQPSFSDER 232
Db 189 ARPPRRGSSRSGD-----AAAAPRRGGKGTQIANCALPCNPFPSQDER 235
QY 233 TF 234
Db 236 AF 237

RESULT 13

US-10-152-548-2
Sequence 2, Application US/10152548
Publication No. US20030040051A1
GENERAL INFORMATION:
APPLICANT: Bhanot, Purnima
APPLICANT: Brink, Marcel
APPLICANT: Harryman, Cindy S.
APPLICANT: Wang, Yanshu
APPLICANT: Heileh, Jen-chih
APPLICANT: Andrew, Deborah
APPLICANT: Nathans, Jeremy
APPLICANT: Nusse, Roel
TITLE OF INVENTION: Wnt Receptor Compositions and Methods
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/152,548
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,340
FILING DATE: 11-APR-1997
APPLICATION NUMBER: US 60/015,307
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0167.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Dfz2 Polypeptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-152-548-2

Query Match 47.4%; Score 621; DB 9; Length 694;
Best Local Similarity 43.4%; Pred. No. 5.1e-42;
Matches 124; Conservative 27; Mismatches 55; Indels 80; Gaps 7;

QY 22 GRAAASAP-----VCOEITVPMCRGIGYNTLTHMPQNFHDTODEAGLEVH 68
Db 40 GHGDASAPAGYVAPALPKDNLNRCIEITIPMCRGIGYNTSFENKMHETODEAGLEVH 99
QY 69 QFWPLVEIQCSFDLRFPLCTMYTPICLPDYHKPLPPCRSVCCERAKAGCSPLMROYGFAMP 128
Db 100 QFWPLVEIQCSFDLRFPLCTMYTPICLEDYKKPLPPCRSVCCERAKAGCAPLMROYGFAMP 159
QY 129 ERMSCDRLPVLRDAEVLICMDY----- 150
Db 160 ERMSCEHPLHG-DPDLNCHQEPSTETASGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGS 218
QY 151 ---NRSEATTAPRPPAKTLDGPPGAPASGGECPAGGFVCKREPPV----- 197
Db 219 GAGSSGSGSTFKPCRGRNSK-NCONPGERAKAGKEG-----CSCRSPLIFLCKEQLQ 271
QY 198 -----PLKESHPLYNKV--RTGVPCAVPCYQPSFSDERTF 235
Db 272 QOSQPMWHHPHWHYNNLTVQRIAGVNCGLPKCGPFPFSDEKDF 317

RESULT 14

US-09-847-102A-43
Sequence 43, Application US/09847102A
Publication No. US20030044409A1
GENERAL INFORMATION:
APPLICANT: University of California
APPLICANT: Carson, Dennis A.
APPLICANT: Cort, Maripat
APPLICANT: Rhee, Chae-Seo
APPLICANT: Lorenzo, Leoni M.

APPLICANT: Malini, Sen
TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
FILE REFERENCE: 22000-20629.00
CURRENT APPLICATION NUMBER: US/09/847,102A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 43
LENGTH: 570
TYPE: PRF
ORGANISM: Drosophila
US-09-847-102A-43

Query Match 44.7%; Score 585; DB 9; Length 570;
Best Local Similarity 48.3%; Pred. No. 3,2e-39;
Matches 117; Conservative 25; Mismatches 52; Indels 48; Gaps 6;

QY 22 GRAAASAP-----VCOETVPMCRGIGYLTMPNQFNHDTQDEAGLEVH 68
DB 29 GHGLDASBPAGVPAIPKDPNLRCBITIPMCRGIGYNTSPFNEMNHETQDEAGLEVH 88
QY 69 QFWPLVETIQSPDLRFPLCTMTYPICLPDYHKPLPCRSVCERAKAGCSPLMRQYGFAMP 128
DB 89 QFWPLVETIKSPDLKFLCSMTYPICLDYHKPLPVCRSVCERARSGCAPIMQYSEFWP 148
QY 129 ERMSCDRLPVGRDAEVLCDY-NRSEATTAPRPFAKPTLPGPAPASG----- 179
DB 149 ERMACENLPLHG-DPDLNLCMQPSYTEAGSGS-----SGSGSGSGSGSGSGGKRRK 198
QY 180 -----GECRAGPFCVCKRBPVILKESHPLYNKRTGQVPCAVPCYQPSFADERT 233
DB 199 QGSGSGSGSGSGSGS-----TSTKPCRGQRGIAGVPCGIRCKGPPFSNDEKD 248
QY 234 FA 235
DB 249 FA 250

RESULT 15

US-09-847-102A-63
Sequence 63; Application US/09847102A
Publication No. US2003004409A1
GENERAL INFORMATION:
APPLICANT: University of California
APPLICANT: Carson, Dennis A.
APPLICANT: Cort, Maripat
APPLICANT: Rhee, Chae-Seo
APPLICANT: Lorenzo, Leonil M.
APPLICANT: Malini, Sen
TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
FILE REFERENCE: 22000-20629.00
CURRENT APPLICATION NUMBER: US/09/847,102A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 63
LENGTH: 244
TYPE: PRF
ORGANISM: Homo sapiens
US-09-847-102A-63

Query Match 36.4%; Score 477; DB 9; Length 244;
Best Local Similarity 41.9%; Pred. No. 5.8e-31;
Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;

QY 3 RPDSPAPPSLLILLIAQLVGRRAAASAPV-----COETVPMCRGIGYLTMPNQF 55
DB 2 RPRSAIPRLILLPLLPAGAPAGQFHGKGISIPDHGFCQIPISIPCTDIAYNOTIMPUL 61
QY 56 NHTQDEAGLEVHQPWPLVETIQSPDLRFPLCTMTYPICLPDYHKPLPCRSVCERAKAG 115

DB 62 GHTNQEDAGLEVHQPWPLVAVKQSPSELRFELCSNYAVCTV-LEQAIIPCRSICERAROG 120
QY 116 CSPIMROYGFAMPERRMSCDRLPVGRDAEVLCDYNRSE-----ATTAPRPFA-KPT 168
DB 121 CEALMKNKFGQWPERLACEHPRHG--AEQICVQNHSEEGAPALTTAP--PGLQPG 175
QY 169 LPGPAPASGGECPAGG---PFVCKRBPVILKESHPLYNKRTGQVPCAVPCYQ 224
DB 176 AGTTPGGPGGGAPPRVATLEHPHCP-----RVLKV--PSYLSYKFLGSRDCAAPC-E 226
QY 225 PS-----FSADERTFA 235
DB 227 PARPDGSMFFSOETRFA 244

Search completed: May 19, 2003, 16:43:39
Job time : 25 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 19, 2003, 16:32:41 ; Search time 20 Seconds

(without alignments)
1129.579 Million cell updates/sec

Title: US-09-847-102a-68

Perfect score: 1310
Sequence: 1 MARPDPSAPSLILLLLAQL.....PNCAPVCYQSPFSADERTFA 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	621	47.4	594	2	Wingless receptor
2	477	36.4	565	2	Fritzzled-2 protein
3	461	35.2	574	2	Fritzzled-7 protein
4	451	34.4	550	2	Wingless protein r
5	415	31.7	647	2	Fritzzled-1 protein
6	399	30.5	641	2	Probable intercell
7	384	29.3	581	2	FZD10 protein - hu
8	370.5	28.3	581	2	gene fritzzled prot
9	366.5	28.0	605	2	hypothetical prote
10	339.5	25.9	568	2	Fritzzled-1 protein
11	334	25.5	197	2	Fritzzled-related p
12	308	23.5	537	2	Fritzzled protein 4
13	297	22.7	666	2	Fritzzled-3 protein
14	282	21.5	706	2	Fritzzled-6 protein
15	270.5	20.6	295	2	Fritzzled protein-2
16	270	20.6	317	2	Fritzzled protein-1
17	218.5	16.7	1113	2	low-density lipopr
18	170	13.0	579	2	membrane-type friz
19	161.5	12.3	526	2	fritzzled protein h
20	140.5	10.7	1774	2	collagen alpha 1(X
21	127.5	9.7	793	2	Smoothed protein
22	106.5	8.1	1955	1	agrin precursor -
23	98.5	7.5	768	2	protein ZC123.1 (I
24	96.5	7.4	211	2	protein F45B8.3 (I
25	96.5	7.4	241	2	hypothetical prote
26	95	7.3	1428	2	lusterin A - Calif
27	94.5	7.2	347	2	hypothetical prote
28	93	7.1	871	1	protein-tyrosine k
29	93	7.1	881	1	protein-tyrosine k

30	93	7.1	1464	2	collagen alpha 1(I
31	92.5	7.1	494	2	zinc finger protei
32	92	7.0	1464	1	collagen alpha 1(I
33	91.5	7.0	303	2	hypothetical prote
34	90	6.9	488	2	collagen alpha 1(I
35	90	6.9	1221	2	fibulin-2 precursor
36	89.5	6.8	674	2	collagen alpha 1(X
37	88.5	6.8	196	2	hibernation-relate
38	88.5	6.8	316	2	hypothetical prote
39	88	6.7	215	2	hibernation-relate
40	87.5	6.7	325	2	hypothetical prote
41	87.5	6.7	396	1	plasma protein Z -
42	87	6.6	510	1	transcription fact
43	86.5	6.6	346	2	hypothetical prote
44	86.5	6.6	700	2	serine/threonine p
45	86	6.6	289	2	thymidylate synth

ALIGNMENTS

RESULT 1

Wingless receptor precursor dfz2 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 02-Mar-2001
C:Accession: S71786; S78444
R:Bhanot, P.; Brink, M.; Harryman Samos, C.; Hsieh, J.C.; Wang, Y.; Macbe, J.P.; Andrew, N.
N:Title: A new member of the fritzzled family from Drosophila functions as a wingless rec
A:Reference number: S71786; MUID:96353971; PMID:8717036
A:Accession: S71786
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-694 <BNA>
A:Cross-References: EMBL:U65589
A:Note: mRNA was also sequenced
R:Bhanot, P.; Wang, Y.; Nathans, J.
submitted to the EMBL Data Library, July 1996
A:Reference number: S78444
A:Accession: S78444
A:Molecule type: DNA
A:Residues: 1-416, 'T', 418-694 <BNM>
A:Cross-References: EMBL:U65589; NID:G1518050; PIDN:AAC42723.1; PID:G1518051
C:Genetics:
A:Gene: dfz2
A:Cross-References: FlyBase:FBgn0016797
A:Superfamily: Fruit fly fritzzled protein
C:Keywords: transmembrane protein

Query Match	47.4%	Score 621;	DB 2;	Length 694;
Best Local Similarity	43.4%	Pred. No. 6.6e-42;		
Matches 124;	Conservative 27;	Mismatches 55;	Indels 80;	Gaps 7;
QY	22	GRAAASKAP-----	VCQEITVPMCRSIGVNLTMPPNQPNHDTODEAGLEVN	68
DB	40	GGGLDASPAHGVGAIPKDPPLRCBEITIPKCRIGVMTSPFPMNHETODEAGLEVN	99	
QY	69	QWPLVETQCSPLDLPFLCTMTYPICLPDYHKPLPPCSVCCRAKAGCSPLMRQYGFAMP	128	
DB	100	QWPLVETQCSPLDLPFLCTMTYPICLPDYHKPLPPCSVCCRAKAGCSPLMRQYGFAMP	159	
QY	129	ERMSCDRLPVGRDDEVICMDY-----		150
DB	160	ERMSCDRLPVGRDDEVICMDY-----		218
QY	151	NRSEATTAPRRFPFPAKPTLPSPGAPASGCECPAGGPFVCKCRBEFV-----		197
DB	219	GAGSGSGSSTSPKCRGRNSK-NQNPQGEKASGKCS-----	CGCRSLPLITLGEKQLQ	271
QY	198	PIKESHPLYNKY---RTGOVPCAVCYQSPFSADERTFA 235		
DB	272	QOSQPMNHHPHMYNLTIVQRIAGVPNCGIPCKGPFPSNDEKPA 317		

RESULT 2

Frizzled-2 protein - human

C:Species: Homo sapiens (man)

C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Mar-2001

C:Accession: J03038

R:Sagara, N.; Toda, G.; Hirai, M.; Terada, M.; Katoh, M.

Biochem. Biophys. Res. Commun. 252, 117-122, 1998

A:Title: Molecular cloning, differential expression, and chromosomal localization of hum

A:Reference number: J03037; PMID:99032814; PMID:9813155

A:Accession: J03038

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-565 <SAG>

A:Cross-references: DDBJ:AB017364; NID:93927884; PIDN:BA34667.1; PID:93927885

C:Superfamily: Fruit fly frizzled protein

Query Match

Best Local Similarity 36.4%; Score 477; DB 2; Length 565;

Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;

QY 3 RPPPSAPPSLLLLLAQLVGRAAAASAPV-----COBITVPMCKGIGYNTLTMNPQF 55

DB 2 RPPSAPRLPLPLPLPMAAPQFHEKGISIPDHGFCQIPISIPLCDIAYNOTIMENL 61

QY 56 NHDTODAGLEVHOFMWPLVEIQCSPDLRFPLCTMYTPICLPDHNKPLPCRSVCERAKAG 115

DB 62 GHTNQBAGLEVHOFMWPLVAVQSPDLRFPLCTMYTPICLPDHNKPLPCRSVCERAKAG 120

QY 116 CSPLMROYGAWPERMSCDRLPVLGRDAEVLCDMYNSE-----ATTAPRPFPRA-KPT 168

DB 121 CEALMKNKFGQWPERLRCEHFRPHG--AEQICVQGNHSEDAVALTLTAPP--PGLQPG 175

QY 169 LPPPGAPASGGECPAG---PPVCKCRFPFPIKESHPLNKKVKTGOVPCAVPCYO 224

DB 176 AGCTPGGPGGGAAPRYATLEHFFHCP-----RLVKV--PSYLSYKFLGERDCAAPC-E 226

QY 225 PS-----PSADERTPA 235

DB 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

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QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 227 PAPPDGSMPFSQEBTRPA 244

QY 105 CRRVCERAVAGCSPLMROYGAWPERMSCDRLPVLGRDAEVLCDMYNSEATTAP---PR 161

DB 120 CRRVCERAVAGCSPLMROYGAWPERMSCDRLPVLGRDAEVLCDMYNSEATTAP---PR 177

QY 162 PPAKPTLPG-----PPGAPASGGECPAGGPFVCKCRFPFPIKESHPLNKKVKTGOV 215

DB 178 APPTAYLDELPTLPPG--ASDGGPAPFPSPC-RQLKVP-----PYIGYRFLGE- 227

QY 216 PPAKPTLPG-----PPGAPASGGECPAGGPFVCKCRFPFPIKESHPLNKKVKTGOV 215

DB 228 RDCGAPC-EPGRANGMYKEERRRA 253

QY 228 RDCGAPC-EPGRANGMYKEERRRA 253

QY 228 RDCGAPC-EPGRANGMYKEERRRA 253

QY 228 RDCGAPC-EPGRANGMYKEERRRA 253

QY 228 RDCGAPC-EPGRANGMYKEERRRA 253

QY 228 RDCGAPC-EPGRANGMYKEERRRA 253

QY 228 RDCGAPC-EPGRANGMYKEERRRA 253

QY 228 RDCGAPC-EPGRANGMYKEERRRA 253

QY 228 RDCGAPC-EPGRANGMYKEERRRA 253

QY 228 RDCGAPC-EPGRANGMYKEERRRA 253

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QY 228 RDCGAPC-EPGRANGMYKEERRRA 253

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QY 228 RDCGAPC-EPGRANGMYKEERRRA 253

QY 228 RDCGAPC-EPGRANGMYKEERRRA 253

QY 228 RDCGAPC-EPGRANGMYKEERRRA 253

QY 228 RDCGAPC-EPGRANGMYKEERRRA 253

QY 228 RDCGAPC-EPGRANGMYKEERRRA 253

QY 228 RDCGAPC-EPGRANGMYKEERRRA 253

Matches 104; Conservative 30; Mismatches 87; Indels 68; Gaps 11;

QY 3 RP--DPSAPPSTLLLL-----AQLVG-PAASAASKAP----- 31

Db 43 RRPVDRRLRLARQLLLMLLEAPLLGLVRAQAAAGCGPGRGCGQPPPPPOOQSGQY 102

QY 32 -----VCEITVPMCRGIGYNTLTHMPNQFNHDTODEAGLEVHQFWPLVEIQCS 79

Db 103 NGERGISVDPDHGQCQISIPDLCTDIYVNOTIMFNLLGHTNQEDAGLEVHQFWPLVVKQCS 162

QY 80 PDRLFLCTMYTPICLPDYHKKLPPCRVSVCERAKAGCSPLMRQYGFAPWRMSCDRLPVL 139

Db 163 AEKFKFLCSYVAVCTV-LEQALPPCRSLCERARQGCCEALMNFQFOWPDLCKEKPVA 221

QY 140 GRDAEVLCDMDYNSSEATTAPRPPFPKPTLPGRPGAPASGCECPAG-----GPFVCKCR 193

Db 222 G--AGELCTCQGNNTSDKGTPTPSLLPFRWTSNPDHGGGHRGFGPGAGASERKFCSP-R 278

QY 194 EPPVPLKESHPLYNKVRGQVNCVPCYOPS-----FSADERTFA 235

Db 279 ALKVPYLYNVHFLGK-----DCGAPC-EPTKYVGLMYFGPELRFS 319

RESULT 6

A:Species: Interleukin 1 signal transducer or transmembrane protein - rat

C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 02-Mar-2001

C:Accession: A45054

R:Chan, S.D.; Karpf, D.B.; Fowlkes, M.E.; Hooks, M.; Bradley, M.S.; Vuong, V.; Bambino, J. Biol. Chem. 267, 25202-25207, 1992

A:Title: Two homologs of the Drosophila polarity gene frizzled (fz) are widely expressed

A:Reference number: A45054; PMID:93094228; PMID:1334084

A:Accession: A45054

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-641 <CH>

A:Experimental source: UMR 106 osteosarcoma cell line

A:Note: sequence extracted from NCBI backbone (NCBI:P120154)

C:Superfamily: fruit fly frizzled protein

Query Match 30.5%; Score 399; DB 2; Length 641;

Best Local Similarity 40.7%; Pred. No. 2,8e-24;

Matches 88; Conservative 28; Mismatches 74; Indels 26; Gaps 8;

QY 33 COEITVPMCRGIGYNTLTHMPNQFNHDTODEAGLEVHQFWPLVEIQCSPLDRFLCTMYTP 92

Db 111 CQISIPDLCTDIYVNOTIMFNLLGHTNQEDAGLEVHQFWPLVVKQCSAEKFKLSMYAP 170

QY 93 ICLPDYHKKLPPCRVSVCERAKAGCSPLMRQYGFAPWRMSCDRLPVLGRDAEVLCDMDYNS 152

Db 171 VCTV-LEQALPPCRSLCERARQGCCEALMNFQFOWPDLCKEKPVAHGRE--LCQGN 226

QY 153 SEATTAPRPPFPKPTLPGRPGAPASGCECPAG-----GPFVCKCRPPVPLKESHPL 206

Db 227 SDKGTPTPSLLPFRWTSNPDHGGGHRGFGPGAGASERKFCSP-RALRVPYLYNVHFL 285

QY 207 YNKVRGQVNCVPCYOPS-----FSADERTFA 235

Db 286 GAK-----DCGAPC-EPTKYVGLMYFGPELRFS 319

RESULT 7

FZD10 protein - human

C:Species: Homo sapiens (man)

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Mar-2001

C:Accession: J07086

R:Koike, J.; Takagi, A.; Miwa, T.; Hirai, M.; Terada, M.; Katoh, M. Biochem. Biophys. Res. Commun. 262, 39-43, 1999

A:Title: Molecular cloning of Frizzled-10, a novel member of the Frizzled gene family.

A:Reference number: J07086; PMID:99382237; PMID:10448064

A:Accession: J07086

A:Molecule type: mRNA

A:Residues: 1-581 <KOI>

A:Cross-references: DDBJ:AB027464; NID:95834487; PIDN:BA84093.1; PID:95834488

A:Experimental source: fetal lung

C:Genetics:

A:Gene: Frizzled-10 (fzd-10)

A:Map position: 12q24.33

C:Superfamily: fruit fly frizzled protein

C:Keywords: glycoprotein; lung; transmembrane protein

Query Match 29.3%; Score 384; DB 2; Length 581;

Best Local Similarity 39.6%; Pred. No. 3.9e-23;

Matches 82; Conservative 27; Mismatches 70; Indels 28; Gaps 7;

QY 1 MARPDPSAPPSTLLLLAQLVGAASAASKAPV-----COEITVPMCRGIGYNTLTHMPN 53

Db 1 MQRPRG-----LMLVLDVMSCAIISMDERPDGKQIETPMCDIGYNTMRMN 54

QY 54 QFNHDTODEAGLEVHQFWPLVEIQCSPLDRFLCTMYTPICLPDYHKKLPPCRVSVCERAK 113

Db 55 LMGHENQREAAIQLHEFAVLEVGCHLRFPLCSLYAPMCTEQVSTPIACRVWCEQAR 114

QY 114 AGCSPLMRQYGFAPWRMSCDRLPVLGRDAEVLCDMD--YNSSEATT-----APR 161

Db 115 LKCSPTMEQFNKRPDPSLDCKRLP-NKNDPNVLCMEAPNNGSDPTRGSGLPPLFRPQR 173

QY 162 PPRKPTLPGRPGAPASGCECPAGGPF 188

Db 174 PHSQGH-PLKCGGPRGS-CDNPKKF 198

RESULT 8

gene frizzled protein precursor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Mar-2001

C:Accession: S03540; S15708; S15709

R:Vinson, C.R.; Conover, S.; Adler, P.N. Nature 338, 263-264, 1989

A:Title: A Drosophila tissue polarity locus encodes a protein containing seven potential

A:Reference number: S03540; PMID:89159415; PMID:2493583

A:Accession: S03540

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-581 <VIN>

A:Radler, P.N.; Vinson, C.; Park, W.J.; Conover, S.; Klein, L. Genetics 126, 401-416, 1990

A:Title: Molecular structure of frizzled, a Drosophila tissue polarity gene.

A:Reference number: S15708; PMID:91060073; PMID:2174014

A:Accession: S15708

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-581 <ADU>

A:Cross-references: EMBL:X54648; NID:97973; PIDN:CAA38460.1; PID:9804979

A:Accession: S15709

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-405, 'MY', 408, 'WQFTIN', <AD2>

A:Cross-references: EMBL:X54648; NID:97973; PIDN:CAA38461.1; PID:9804980

C:Genetics:

A:Gene: FlyBase:fz

A:Cross-references: FlyBase:FBgn0001085

A:Introns: 224/3; 264/3; 329/3; 405/1

C:Superfamily: fruit fly frizzled protein

C:Keywords: alternative splicing; transmembrane protein

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-581/Product: gene frizzled protein #status predicted <MAT>

Query Match 28.3%; Score 370.5; DB 2; Length 581;

Best Local Similarity 41.1%; Pred. No. 4.7e-22;

Matches 85; Conservative 29; Mismatches 72; Indels 21; Gaps 9;

QY 33 COEITVPMCRGIGYNTLTHMPNQFNHDTODEAGLEVHQFWPLVEIQCSPLDRFLCTMYTP 92

```

      53 CEBITISICKINIPNTIMNLIGHTQEBAGLEVHQFADLVKIGCDDDLFLCISLYVP
      93 ICPDHYHKLPPCRSVCEBAKAGCSPLMROYGFAMPERMSCDRLPYLGRDAEVLQCMYNN-
      113 VC-TILERPLPPCGLCSARV-CEKLMKTYNFMWPNENLECSKFPVAG--GEDLCVAENT
      152 -RSEATTAPRPPRPAPKPTLPGRPPAPASGSGCPAGG-PFYCKCREPVPPI-LKESHPLYN
      169 TSSASTAATRTSAKYAT-----TRKHOTGVESPFRNIGFVC-----PVLKTPILMGY
      209 KVRGTG--QVENCAPVCYQPSFSADERT 223
      218 ELKVGKDLHDGCAFCAMFFPERERT 244

```

RESULT 9

```

T31690
Hypothetical protein F27E11.3 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 02-Mar-2001
C/Accession: T31690
R/Name: P. J. Keppeler, D.
Submitted to the EMBL Data Library, July 1997
A/Description: The sequence of C. elegans cosmid F27E11.
A/Reference number: Z21069
A/Accession: T31690
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-605 <WAM>
A/Cross-references: EMBL:AF016413; PIDN:AB65257.1; GSPDB:GN00023; CESP:F27E11.3
A/Experimental source: strain Bristol N2; clone F27E11
C/Genetics:
A/Map position: 5
A/Intons: 28/3; 454/1; 520/1; 562/1
C/Superfamily: fruit fly frizzled protein

```

Query Match

Best local Similarity 28.0%; Score 366.5; DB 2; Length 605;
Matches 76; Conservative 25; Mismatches 66; Indels 35; Gaps 5;

```

QY 48 LTHMNFNDTODEAGLEVHQFAMPLVEIQSPDLRFLCTMYTPTCLPDYHKLPPCRS
      1 MTFEPNYSYGHKEQEALEVHQFPLVEVCGFQHLKFLCTMYTPTICQENVDKILPCME
      108 VCBRAKAGCSPLMROYGFAMPERMSCDRLPYLGRDAEVLQCMYNNRSEATTAPRPPR
      61 LCVEBAKSCSPIMAKYGFAMPTLSCALPKMS-----DOMSTNICAPPDTRKKQ
      168 -----TLGPP- GAPASGSGCPAGG-GPFVCKCREPVPPI-LKESHP
      113 HKGHHKNNQNNQNNNNYSPDGEVGISKIDNEVINGPSQCCTCNGPQFVASE-----
      207 YNKVRGTGQVENCAPVCYQPSFS 228
      169 --KSKVGNVTNCAVSCHPAL 188

```

RESULT 10

```

T25162
Frizzled-1 protein homolog - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Mar-2001
C/Accession: T25162; T42210
R/Name: A.
Submitted to the EMBL Data Library, October 1996
A/Reference number: Z19989
A/Accession: T25162
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-566 <WIL>
A/Cross-references: EMBL:Z81128; PIDN:CAB03398.1; GSPDB:GN00019; CESP:T23D8.1

```

```

A/Experimental source: clone T23D8
R/Bochleau, C.E.; Downs, W.D.; Lin, R.; Wiltmann, C.; Bei, Y.; Cha, Y.H.; Ali, M.; Prie
      Cell 90, 707-716, 1997
A/Title: Wnt signaling and an APC related gene specify endoderm in early C. elegans embri
A/Reference number: Z15051; MUID:97433081; PMID:9288750
A/Accession: T42210
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-566 <ROC>
A/Cross-references: EMBL:AF013953; NID:G2463673; PIDN:AAC47750.1; PID:G2463674
C/Genetics:
A/Map position: 1
A/Intons: 158/2; 280/1; 326/2; 407/1; 447/2; 520/2
C/Superfamily: fruit fly frizzled protein

```

Query Match 25.9%; Score 339.5; DB 2; Length 568;
Best local Similarity 34.0%; Pred. No. 1.3e-19;
Matches 69; Conservative 35; Mismatches 56; Indels 43; Gaps 7;

```

QY 33 COBITVPMCRGIGYNTLTHMNFNDTODEAGLEVHQFAMPLVEIQSPDLRFLCTMYTP
      37 CEHITPMCKNDYNGTVFENLGHITQSEAGPALAQFNPLIKVKSSEDIRLFLCTVAP
      93 ICPDHYHKLPPCRSVCEBAKAGCSPLMROYGFAMPERMSCDRLPYLGRDAEVLQCMYNN
      97 VCTV-LEKPIQPCRELCLSAKNGCESLMKKFGQWPDOLDCKNFPTD-----LCVGNKS
      153 SEATTAPRPPRPAPKPTLPGRPPAGSGE-----CP-----AGPFCCKREPVPPI
      151 SESSNS-----KSSNDVTFGVSTIANEVVUSPKKCPHMTTSGSH-----SLPL
      200 LKESHPLYNKKVRTGOVENCAPVC 222
      198 L-----SGRLPECSLTC 209

```

RESULT 11

JC7735

```

Frizzled-related protein - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 14-Dec-2001
C/Accession: JC7735
R/Yam, J.W.P.; Chan, K.W.; Wong, V.K.W.; Hsiao, W.L.W.
Biochem. Biophys. Res. Commun. 286, 94-100, 2001
A/Title: Transcriptional activity of the promoter region of rat frizzled-related protein
A/Reference number: JC7735; MUID:21378144; PMID:11485313
A/Accession: JC7735
A/Molecule type: DNA
A/Residues: 1-197 <YAM>
A/Cross-references: GB:AF140347
C/Comment: This protein is a new family of secreted proteins involved in tumorigenesis a
A/Genes: rFrp
A/Intons: 148/3; 175/3

```

Query Match

Best local Similarity 25.5%; Score 334; DB 2; Length 197;
Matches 69; Conservative 31; Mismatches 65; Indels 32; Gaps 5;

```

QY 15 LLIAOLVG-----RAAASKAPVCEITVPMCRGIGYNTLTHMNFNDTODEAGLEVHQ
      1 MLISIVALLCLWLRLALGVAGPCEAVRIPMCHMPMNITRMNHLHSTQENVALIAIQ
      70 FFWLVIQSPDLRFLCTMYTPTCLPDY-HKPLPPCRSVCEBAKAGCSPLMROYGFAMP
      61 YEELVDVNCSSVLSFPLCMYAPICTLEPLHDPIKCKSVCCQARDCSEPLMGMVHNSW
      129 ERMSCDRLPVLRG-----DAEVLQCM-----YNRSEATTAPRPPRPAPKPTLPGR
      121 ESLACDELVPYDRGVGISSEALVTDLPEDVKMIDIRPDMVNGERSDA-----
      178 SGGECPAGGPFVCKRE 194

```

Db 169 ---DCKHLSRDRCKCK 182

RESULT 12

frizzled protein 4 - human

C:Species: Homo sapiens (man)

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001

C:Accession: J07127

R:Kirkkholi, H.; Sagara, N.; Koike, J.; Tanaka, K.; Sekihara, H.; Hirai, M.; Katoh, M.

Biochem. Biophys. Res. Commun. 264, 955-961, 1999

A:Title: Molecular cloning and characterization of human frizzled-4 on chromosome 11q14-

A:Reference number: J07127; PMID:10544037

A:Accession: J07127

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-537 <KIR>

A:Cross-references: GB:AB032417; DDBJ:AB032417; NID:96277265; PID:96277266

A:Gene: FZD4

A:Map position: 11 region q14 - q21

C:Superfamily: fruit fly frizzled protein

Query Match 23.5%; Score 308; DB 2; Length 537;

Best Local Similarity 34.0%; Pred. No. 4e-17;

Matches 64; Conservative 33; Mismatches 71; Indels 20; Gaps 5;

6 PSAPSL-----LLLLLAQV--RAAASKAVCOEITVPMCRGIGYNTLHMPQENHD 58

Db 11 PGAPGGVGLSLGLLQLLLPARGFGDEERRCPDIRISMCONIGYNTKPNLVGHE 70

59 TODEAGLEVHQPFWLVEIQSPDLRFPLCTMYTPICLPDYHKEPLPCRSVCERAKACSP 118

Db 71 LQTDALQLQTLTFPLQYQSSQLQFLCSVYPMCTEKNINIGCGMCLSVKRCER 130

QY 119 LMRQYFANPERNSCDRLPYLGDAEVLCHDYRSEATTAAPRPFPKPTLPGPAPAS 178

Db 131 VLKEFPFAPBESINCSKFP--QNDHNMCMEGGDEEVPPLPHKT--PIQP----- 177

QY 179 GGECPAGG 186

Db 178 GEECHSVG 185

RESULT 13

J07312

frizzled-3 protein - human

C:Species: Homo sapiens (man)

C:Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 02-Mar-2001

C:Accession: J07312

R:Salz, C.F.; Formenti, E.; Terstappen, G.C.; Caricasole, A.

Biochem. Biophys. Res. Commun. 273, 27-34, 2000

A:Title: Identification, gene structure, and expression of human frizzled-3 (FZD3).

A:Reference number: J07312

A:Accession: J07312

A:Molecule type: mRNA

A:Residues: 1-666 <SAL>

A:Cross-references: GB:A127242

A:Experimental source: brain

C:Comment: This protein, a seven-transmembrane receptor belonging to the frizzled family

possit101 levels in cells.

A:Gene: fzds

A:Map position: 8p21

C:Superfamily: fruit fly frizzled protein

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 22.7%; Score 297; DB 2; Length 666;

Best Local Similarity 35.5%; Pred. No. 3.7e-16;

Matches 75; Conservative 23; Mismatches 69; Indels 44; Gaps 9;

Db 28 CEPITLRMCQDLPYNTTFEPNLLNHYDQFTALANEPFPMVNLDCSRFPFLCALVAP 87

QY 93 ICLPDYHKEPLPCRSVCERAKACSPLMRQYGFAMPERNSCDRLPYLGDAEVLCHDYR 152

Db 88 ICM-EYGRVTLFCRRLCQAYISECSKLMEMFVPMPEDECSRFP-----DCD----- 134

QY 153 SBATTAPRRFPKPTLPGP--GAPAS-----GGECPAGGPFVCKRBPVPLKESH 205

Db 135 -----EPYRRLVDNLAGEPREGAPVAVQRYGFWCP-----RE-----LKIDPD 174

QY 206 L-YMKRTQVPCAVPCYQSPFSADERTFA 235

Db 175 LGYSFL---HVDCSPPCPNMYFRRELSFA 202

RESULT 14

J0164

frizzled-6 protein precursor - human

C:Species: Homo sapiens (man)

C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 02-Mar-2001

C:Accession: J0164

R:Tokuhara, M.; Hirai, M.; Atomi, Y.; Terada, M.; Katoh, M.

Biochem. Biophys. Res. Commun. 243, 622-627, 1998

A:Title: Molecular cloning of human frizzled-6.

A:Reference number: J0164; PMID:9480858

A:Accession: J0164

A:Molecule type: mRNA

A:Residues: 1-706 <TOK>

A:Cross-references: GB:AB012911; NID:93062802; PID:NBA25686.1; PID:93062803

C:Comment: This protein is receptor for selected glycoproteins in development and carcin

C:Genetics:

A:Gene: Hfz6

A:Map position: 8q22.3-q23.1

C:Superfamily: fruit fly frizzled protein

C:Keywords: glycoprotein

F:1-18/Domain: signal sequence #status predicted <SIG>

F:201-222/Domain: transmembrane #status predicted <TM1>

F:233-255/Domain: transmembrane #status predicted <TM2>

F:281-312/Domain: transmembrane #status predicted <TM3>

F:324-345/Domain: transmembrane #status predicted <TM4>

F:370-393/Domain: transmembrane #status predicted <TM5>

F:417-436/Domain: transmembrane #status predicted <TM6>

F:473-495/Domain: transmembrane #status predicted <TM7>

F:38,352/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.5%; Score 282; DB 2; Length 706;

Best Local Similarity 30.8%; Pred. No. 6.1e-15;

Matches 65; Conservative 22; Mismatches 80; Indels 44; Gaps 6;

33 COEITVPMCRGIGYNTLHMPQENHDQDEAGLEVHQPFWLVEIQSPDLRFPLCTMYTP 92

Db 24 CEPITVPMCRKAYNTTFFPNLMGHYDQSIAAVEHNFPLPLNLESPYIFLCAFP 83

QY 93 ICLPDYHKEPLPCRSVCERAKACSPLMRQYGFAMPERNSCDRLPYLGDAEVLCHDYR 152

Db 84 TCIEQIH-VVPCRKLCXKVSDDCKLIDTPIGRMBELECRLQYCDRTVPY----- 135

QY 153 SEATTAPRRFP--PAKPTLPGPAPASGGECPAGGPFVCKRBPVPLKESHPLYNKY 210

Db 136 ---TFDPTHTFAGPOKKT-----EYQVORDIGFWC-----PHLTKT 167

QY 211 RTGQ-----VNCAPVCYQSPFSADERTFA 235

Db 168 SGGQGYKFLIGDIOCAPPCPNMYFKSDELEFA 198

RESULT 15

J0174

frizzled protein-2 - human

C:Species: Homo sapiens (man)

C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999

C:Accession: J0174

R:Hu, E.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.
 Biochem. Biophys. Res. Commun. 247, 287-293, 1998

A:Title: Tissue restricted expression of two human frzbs in preadipocytes and pancreas.
 A:Reference number: JE0174; MID:98308108; PMID:9642118

A:Accession: JE0174

A:Molecule type: mRNA

A:Residues: 1-295 <HUA>

C:Genetics:

A:Map position: 4q

Query Match 20.6%; Score 270.5; DB 2; Length 295;

Best Local Similarity 36.3%; Pred. No. 2.2e-14;

Matches 62; Conservative 26; Mismatches 60; Indels 23; Gaps 7;

```

QY 9 PPSLLLLLLAO-----LVGRAAAASKAPVCOEI--TVPMCRGIGYNLTHMPNOF 55
DB 5 PPSLLLLFLASHCHCLSGARGLFLFGQPDFSYKRSNCKPIRANLQLCHGIEYQNRLEPNLL 64
QY 56 NMDTQDEAGLEVHQFW-PLVEIQSPDLRPFELCTMTYTPICLPDYHKPLPCCRVCERAKA 114
DB 65 GHETMKKEV-LEQAGAWIPLVWKQCHPDTKKFLCSLFAVCLDDDETITQCHSLCVQVKD 123
QY 115 GCSPLMQYGFAMPERRMSCDRLPVLGRDAEVLCDYNRSE----ATAPRR 161
DB 124 RCAFVMSAFGFWPMDMLECDRFP---QDND-LCIPILASDHLPLPATEAPK 170

```

Search completed: May 19, 2003, 16:34:58

Job time : 24 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2003, 16:32:11 ; Search time 13 Seconds
(without alignments)
749.764 Million cell updates/sec

Title: US-09-847-102a-68

Perfect score: 1310
Sequence: 1 MARPPSAPPSLLLLLLAQL.....PNCAPVCYQPSFSADERTFA 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1310	100.0	585	FZD5_HUMAN	013467 homo sapien
2	1143	87.3	577	FZD5_MOUSE	096d0 mus musculu
3	825.5	63.0	559	FZD5_XENLA	P58421 xenopus lae
4	824	62.9	694	FZD8_HUMAN	09h461 homo sapien
5	823.5	62.9	681	FZD8_MOUSE	061091 mus musculu
6	802	61.2	585	FZD8_XENLA	093374 xenopus lae
7	621	47.4	694	FRZ2_DROME	09vrx3 drosophila
8	477	36.4	565	FZD2_HUMAN	014332 homo sapien
9	476	36.3	570	FZD2_MOUSE	09j1p6 mus musculu
10	466	35.6	574	FZD2_RAT	008464 rattus norv
11	457	34.9	570	FZD7_HUMAN	075084 homo sapien
12	440.5	33.6	572	FZD7_MOUSE	061090 mus musculu
13	438.5	33.5	551	FZD2_XENLA	09pu6 xenopus lae
14	431	32.9	592	FZD1_CHICK	057328 gallus gall
15	422	32.2	642	FZD1_MOUSE	070421 mus musculu
16	421	32.1	523	FZD2_CHICK	091628 gallus gall
17	414.5	31.6	648	FZD1_HUMAN	09up38 homo sapien
18	411	31.4	567	FZD1_CHICK	057328 gallus gall
19	405.5	31.0	559	FZD7_XENLA	09pu8 xenopus lae
20	401	30.6	549	FZD1_MOUSE	0918m5 xenopus lae
21	398	30.4	641	FZD1_RAT	008465 rattus norv
22	394.5	30.1	591	FZD9_HUMAN	000144 homo sapien
23	394.5	30.1	592	FZD9_MOUSE	09r1w6 mus musculu
24	384	29.3	581	FZ10_HUMAN	09u126 homo sapien
25	372	28.4	325	FRZB_HUMAN	092765 homo sapien
26	371	28.3	583	FRIZ_DROVI	024760 drosophila
27	370.5	28.3	581	FRIZ_DROME	P18537 drosophila
28	368	28.1	586	FZD4_XENLA	09d8b5 xenopus lae
29	367	28.0	323	FRZB_MOUSE	P97401 mus musculu
30	366	27.9	325	FRZB_BOVIN	095117 bos taurus
31	360	27.5	580	FZD8_XENLA	09w742 xenopus lae
32	351	26.8	585	FZD8_CHICK	09puh2 gallus gall
33	309	23.6	523	FZD4_XENLA	09pl62 xenopus lae

34	308	23.5	537	1	FZD4_HUMAN	09ulv1 homo sapien
35	304.5	23.2	666	1	FZD3_MOUSE	061086 mus musculu
36	302.5	23.1	525	1	FZD4_CHICK	091a05 gallus gall
37	300.5	22.9	538	1	FZD4_RAT	09qzho rattus norv
38	299.5	22.9	537	1	FZD4_MOUSE	061088 mus musculu
39	297	22.7	666	1	FZD3_HUMAN	09np21 homo sapien
40	293.5	22.4	664	1	FZD3_XENLA	042579 xenopus lae
41	284	21.7	705	1	FRZ4_DROME	09hdw1 drosophila
42	282	21.5	706	1	FZD6_HUMAN	060353 homo sapien
43	271	20.7	709	1	FZD6_MOUSE	061089 mus musculu
44	261	19.9	581	1	FRZ3_DROME	077438 drosophila
45	218.5	16.7	1113	1	CORT_MOUSE	092319 mus musculu

ALIGNMENTS

RESULT 1
FZD5_HUMAN STANDARD; PRI; 585 AA.
ID FZD5_HUMAN
AC 013467;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fzizzled 5 precursor (Fzizzled-5) (Fz-5) (Fz5) (Fz5).
GN FZD5 OR HFZ5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=96224032; PubMed=8626800;
RA Wang Y., Mcke J.P., Abella B.S., Andreasen K., Worley P.,
Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.,
RT "A large family of putative transmembrane receptors homologous to the
product of the Drosophila tissue polarity gene frizzled.";
RL J. Biol. Chem. 271:4468-4476(1996).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=21301556; PubMed=11408929;
RA Satoh T., Hirai M., Katoh M.,
RT "Molecular cloning and characterization of human Fzizzled-5 gene on
chromosome 2q33.3-q34 region.";
RL Int. J. Oncol. 19:105-110(2001).
RN (3)
RP SEQUENCE OF 273-331 FROM N.A.
RC TISSUE=oesophageal carcinoma;
RX MEDLINE=98374323; PubMed=9707618;
RA Tanaka S., Akiyoshi T., Mori M., Wada J.R., Sugimachi K.,
RT "A novel frizzled gene identified in human esophageal carcinoma
mediate APC/beta-catenin signals.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:10164-10169(1998).
RN (4)
RP COUPLING TO BETA-CATENIN PATHWAY.
RX MEDLINE=97207341; PubMed=9054360;
RA He X., Saint-Jeanne J.P., Wang Y., Nathans J., David I., Varmus H.,
RT "A member of the Fzizzled protein family mediating axis induction by
Wnt-5A.";
RL Science 275:1652-1654(1997).
-1-
FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
are coupled to the beta-catenin canonical signaling pathway, which
leads to the activation of dishevelled proteins, inhibition of
GSK-3 kinase, nuclear accumulation of beta-catenin and activation
of Wnt target genes. A second signaling pathway involving PKC and
calcium fluxes has been seen for some family members, but it is
not yet clear if it represents a distinct pathway or if it can be
integrated in the canonical pathway, as PKC seems to be required
for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
to involve interactions with G-proteins. May be involved in
transduction and intercellular transmission of polarity
information during tissue morphogenesis and/or in differentiated

```

CC tissues. Interacts specifically with wnt5a to induce the beta-
CC catenin pathway.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DOMAIN: Lys-Thr-X-X-Tyr motif is involved in the activation of
CC the Wnt/beta-catenin signaling pathway (by similarity) (By
CC similarity).
CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
CC RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
CC -----
CC .This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U43318; AAC50385.1; -
CC EMBL; AB043702; BAB60959.1; -
CC Gene; HGNC:4043; FZD5.
CC MIM; 601723; -
CC DR InterPro; IPR000539; Frizzled.
CC DR InterPro; IPR000024; Fz_domain.
CC DR InterPro; IPR000832; GPCR_secretin.
CC DR Pfam; PF01392; Fz; 1.
CC DR Pfam; PF01534; Frizzled; 1.
CC DR PRINTS; PRO0489; FRIZZLED.
CC DR SMART; SM00063; FRI; 1.
CC DR PROSITE; PSS0038; FZ; 1.
CC DR PROSITE; PSS0261; G_PROTEIN_RECPT_P2_4; 1.
CC DR Multigene family; G-protein coupled receptor; Transmembrane;
CC KM Developmental protein; Glycoprotein; Signal.
CC FT SIGNAL 1 26
CC FT CHAIN 27 585
CC FT DOMAIN 27 238
CC FT TRANSMEM 239 259
CC FT DOMAIN 260 270
CC FT TRANSMEM 271 291
CC FT DOMAIN 292 315
CC FT TRANSMEM 316 336
CC FT DOMAIN 337 358
CC FT TRANSMEM 359 379
CC FT DOMAIN 380 402
CC FT TRANSMEM 403 423
CC FT DOMAIN 424 449
CC FT TRANSMEM 450 470
CC FT DOMAIN 471 500
CC FT TRANSMEM 501 521
CC FT DOMAIN 522 585
CC FT TRANSMEM 523 530
CC FT SITE 525 530
CC FT SITE 583 585
CC FT CARBOHYD 47 47
CC FT CARBOHYD 151 151
CC FT CONFLICT 88 263
CC FT CONFLICT 262 263
CC FT CONFLICT 345 345
CC FT CONFLICT 357 357
CC FT CONFLICT 402 402
CC SQ SEQUENCE 585 AA; 64551 MW; CF66C5BA746E7971 CRC64;
Query Match 100.0%; Score 1110; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.8e-95;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARPDSAPSLILLILLAQVGRRAAASKAPVCOEITVPMCRGIGYNTLTMNQFNHDQ 60
DB 1 MARPDSAPSLILLILLAQVGRRAAASKAPVCOEITVPMCRGIGYNTLTMNQFNHDQ 60
QY 61 DEAGLEVHGFVLPVLEIQCSDDLRFLLCTMTPTPICLPDYHKPLPPCRSVCEKARAGCSPLM 120
DB 61 DEAGLEVHGFVLPVLEIQCSDDLRFLLCTMTPTPICLPDYHKPLPPCRSVCEKARAGCSPLM 120

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```

DB 61 DEAGLEVHGFVLPVLEIQCSDDLRFLLCTMTPTPICLPDYHKPLPPCRSVCEKARAGCSPLM 120
QY 121 ROYGFAMPFRMSCDRLPVGLRDAEVLICMDYNRSEATTAPRPFPAPKPTLPGPGAGASG 180
DB 121 ROYGFAMPFRMSCDRLPVGLRDAEVLICMDYNRSEATTAPRPFPAPKPTLPGPGAGASG 180
QY 181 ECPAGGPFVCKCEPFPVPLIKESHPLYNKRTGVNCAVPCYQSPFSADERTFA 235
DB 181 ECPAGGPFVCKCEPFPVPLIKESHPLYNKRTGVNCAVPCYQSPFSADERTFA 235
RESULT 2
FZD5_MOUSE STANDARD; PRT; 577 AA.
ID FZD5_MOUSE
AC Q9EBD0; O08975;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Frizzled 5 precursor (Frizzled-5) (Fz-5) (mFz5).
GN FZD5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6N; TISSUE=Gut;
RX PubMed=11092808;
RA Ishikawa T., Tamai Y., Zorn A.M., Yoshida H., Seldin M.F.,
RA Nishikawa S.-I., Takeo M.M.;
RT "Mouse Wnt receptor gene Fzd5 is essential for yolk sac and placental
RL development 128:25-33(2001).
RN [2]
RP SEQUENCE OF 207-286 FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Prostate;
RA Johnson M.A., Greenberg N.M.;
RL Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP TISSUE SPECIFICITY.
RX MEDLINE=96224032; PubMed=8626800;
RA Wang Y., Macke J.P., Abella B.S., Andreasson K., Worley P.,
RA Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;
RT "A large family of putative transmembrane receptors homologous to the
RL product of the Drosophila tissue polarity gene frizzled.";
J. Biol. Chem. 271:4468-4476(1996).
CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
CC are coupled to the beta-catenin canonical signaling pathway, which
CC leads to the activation of dishevelled proteins, inhibition of
CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
CC of Wnt target genes. A second signaling pathway involving PKC and
CC calcium fluxes has been seen for some family members, but it is
CC not yet clear if it represents a distinct pathway or if it can be
CC integrated in the canonical pathway, as PKC seems to be required
CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
CC to involve interactions with G-proteins. May be involved in
CC transduction and intercellular transmission of polarity
CC information during tissue morphogenesis and/or in differentiated
CC tissues. Plays a role in yolk sac angiogenesis and in placental
CC vascularization. Binds to Wnt2, Wnt10B, Wnt5A, but not to Wnt2B or
CC Wnt4.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in eye, kidney, lung, chondrocytes,
CC epithelial cells of the small intestine and goblet cells of the
CC colon.
CC -1- DEVELOPMENTAL STAGE: Expressed in the yolk sac, placenta, eye and
CC lung bud at 9.5 days post coitum (dpc). At 10.5 dpc, also
CC expressed in the placental blood vessel of embryonic origin.
CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
CC RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

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DR EMBL AF272146; AAC39355.1; -
 DR EMBL AF005203; AAC01953.1; -
 DR MGD: MGI:108571; Pzds.
 DR InterPro: IPR000539; Frizzled.
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR000832; GPCR_secretin.
 DR Pfam: PF01392; Fz; 1.
 DR Pfam: PF01534; Frizzled; 2.
 DR PRINTS: PR00489; FRIZZLED.
 DR SMART: SM00063; FRI; 1.
 DR PROSITE: PS50038; Fz; 1.
 DR PROSITE: PS50261; G-PROTEIN RECEPTOR F2_4; 1.
 DR Multigene family; G-protein coupled receptor; Transmembrane;
 DR Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 577
 FT DOMAIN 27 234
 FT TRANSMEM 235 255
 FT DOMAIN 256 266
 FT TRANSMEM 267 287
 FT DOMAIN 288 311
 FT TRANSMEM 312 332
 FT DOMAIN 333 354
 FT TRANSMEM 355 375
 FT DOMAIN 376 398
 FT TRANSMEM 399 419
 FT DOMAIN 420 445
 FT TRANSMEM 446 466
 FT DOMAIN 467 495
 FT TRANSMEM 496 516
 FT DOMAIN 517 577
 FT DOMAIN 578 598
 FT SITE 575 577
 FT CARBOHYD 47 47
 FT CARBOHYD 151 151
 SQ SEQUENCE 577 AA; 63794 MW; F6877C9B535C865 CRC64;

Query Match
 Best Local Similarity 87.3%; Score 1143; DB 1; Length 577;
 Matches 214; Conservative 3; Mismatches 14; Indels 4; Gaps 3;

OY 1 MARPPSAPPSLLLLLLAOLVGRRAAASAPVCOEITVPMCRGIGYNLTTHMPQFNHTQ 60
 DB 1 MARPPSAPPSLLLLLLAOLVGRRAAASAPVCOEITVPMCRGIGYNLTTHMPQFNHTQ 60
 OY 61 DEAGLEVHOFWPLVETIQCSBDLRFLLCTMYTPICLPDYHKPLPPCCSVCERAYAGCSPLM 120
 DB 61 DEAGLEVHOFWPLVETIQCSBDLRFLLCTMYTPICLPDYHKPLPPCCSVCERAYAGCSPLM 120
 OY 121 ROYGFAPWRMSGCDRLPVYGRDAEVLCMDYNSEATAPRRPAPRPTLPGPFGAASAG 180
 DB 121 ROYGFAPWRMSGCDRLPVYGRDAEVLCMDYNSEATAPRRPAPRPTLPGPFGAASAG 180
 OY 181 ECPAGAPFVCKREPFPVPLIKESHPLYNKVRITGOVNCACVPCQSPFSADERTFA 235
 DB 181 ECPAGAPFVCKREPFPVPLIKESHPLYNKVRITGOVNCACVPCQSPFSADERTFA 235
 DB 180 ECGSHRQVS--EPFVPLIKESHPLYNKVRITGOVNCACVPCQSPFSADERTFA 231

RESULT 3
 ID FZDS_XENIA STANDARD; PRT; 559 AA.
 AC P58421;
 DT 15-JUN-2002 (rel. 41, Created)
 DT 15-JUN-2002 (rel. 41, Last sequence update)

DT 15-JUN-2002 (rel. 41, Last annotation update)
 GN Frizzled 5 precursor (Frizzled-5) (Fz-5) (Xfz5).
 DE FZ5.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21233029; PubMed=11335120;
 RA Sumana S., Ekker S.C.,
 RT "Xenopus frizzled-5: a frizzled family member expressed exclusively in
 RL the neural retina of the developing eye.";
 Mech. Dev. 103:133-136(2001).
 CC -! FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 CC are coupled to the beta-catenin canonical signaling pathway, which
 CC leads to the activation of dishevelled proteins, inhibition of
 CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 CC of Wnt target genes. A second signaling pathway involving PKC and
 CC calcium fluxes has been seen for some family members, but it is
 CC not yet clear if it represents a distinct pathway or if it can be
 CC integrated in the canonical pathway, as PKC seems to be required
 CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 CC to involve interactions with G-proteins. May be involved in
 CC transduction and intercellular transmission of polarity
 CC information during tissue morphogenesis and/or in differentiated
 CC tissues.
 CC -! SUBCELLULAR LOCATION: Integral membrane protein.
 CC -! TISSUE SPECIFICITY: Expressed in retina.
 CC -! DEVELOPMENTAL STAGE: First detected at the late neurula stage in
 CC retinal primordia. Throughout the tailbud stage, expressed
 CC exclusively in the neural retina within the optic vesicles. During
 CC tadpole stage, expression becomes restricted to the ciliary
 CC marginal zone.
 CC -! DOMAIN: Lys-Thr-X-X-X-Tyr motif is involved in the activation of
 CC the Wnt/beta-catenin signaling pathway (By similarity).
 CC -! DOMAIN: The fz domain is involved in binding with Wnt ligands (By
 CC similarity).
 CC -! SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC -! SIMILARITY: CONTRAINS 1 FRIZZLED (FZ) DOMAIN.
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 CC or send an email to license@isb-sib.ch).

DR EMBL AF00716; AAK51688.1; -
 DR InterPro: IPR000539; Frizzled.
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR000832; GPCR_secretin.
 DR Pfam: PF01392; Fz; 1.
 DR Pfam: PF01534; Frizzled; 1.
 DR PRINTS: PR00489; FRIZZLED.
 DR SMART: SM00063; FRI; 1.
 DR PROSITE: PS50038; Fz; 1.
 DR PROSITE: PS50261; G-PROTEIN RECEPTOR F2_4; 1.
 DR Multigene family; G-protein coupled receptor; Transmembrane;
 DR Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 559
 FT DOMAIN 27 220
 FT TRANSMEM 221 241
 FT DOMAIN 242 257
 FT TRANSMEM 258 278
 FT DOMAIN 279 301
 FT TRANSMEM 302 322
 FT DOMAIN 323 343
 FT TRANSMEM 344 364

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FT DOMAIN 365 387 EXTRACELLULAR (POTENTIAL)
FT TRANSMEM 388 408 5 (POTENTIAL)
FT DOMAIN 409 434 CYTOPLASMIC (POTENTIAL)
FT TRANSMEM 435 455 6 (POTENTIAL)
FT DOMAIN 456 483 EXTRACELLULAR (POTENTIAL)
FT TRANSMEM 484 504 7 (POTENTIAL)
FT DOMAIN 505 559 CYTOPLASMIC (POTENTIAL)
FT DOMAIN 528 149 FZ.
FT DOMAIN 152 157 LYS-THR-X-X-TRP MOTIF.
FT SITE 507 512 PDZ-BINDING.
FT SITE 557 559 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 468 468 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 559 AA; 63518 MW; 581EB243FCB954B7 CRC64;

Query Match 63.0%; Score 825.5; DB 1; Length 559;
Best Local Similarity 69.2%; Pred. No. 1.3e-57;
Matches 153; Conservative 20; Mismatches 35; Indels 13; Gaps 4;

QY 14 LLLLAQLVGRRAAASKAPVCEITVPMCRGIGYVLTMPNPFNDTODEAGLEVHGFMP 73
DB 14 VVLLDVFAPAQAASKAIIVCEITVPMCRGIGYVLTMPNPFNDTODEAGLEVHGFMP 73
QY 74 VETQSPDLRFPLCTMTPTICLPDYHKLPPCSVCERAAAGCSPLMRYGFAMPERMSC 133
DB 74 VVIQCSIDLKFLCSMTPTICLPDYHKLPPCSVCERAAAGCSPLMRYGFAMPERMSC 133
QY 134 DRIPVLRGDAVLCMDVNRSEATAPRPPAKPTLPGPPGAPASSGECAGAGPFVCKR 133
DB 134 DRIPERHG-DDPTLCMYNMTETTTTP-----PTHPPKVKTPS--DCDG---VCKCR 180
QY 194 EPEVPIKESHPLYNKRVQGVNCAVPCYQSPESADERTF 234
DB 181 EPEVITRESHPLYNKRVQGVNCAVPCYQSPESADERTF 221

RESULT 4
FZD8 HUMAN STANDARD; PRT; 694 AA.
AC 09H461;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Frizzled 8 precursor (Frizzled-8) (Fz-8) (hFz8).
GN FZD8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21192958; PubMed=11295046;
RA Saitoh T., Hirai M., Katoh M.;
RT "Molecular cloning and characterization of human Frizzled-8 gene on
RL chromosome 10p11.2."
RL Int. J. Oncol. 18:991-996 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Heath P.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
CC are coupled to the beta-catenin canonical signaling pathway, which
CC leads to the activation of dishevelled proteins. Inhibition of
CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
CC of Wnt target genes. A second signaling pathway involving PKC and
CC calcium fluxes has been seen for some family members, but it is
CC not yet clear if it represents a distinct pathway or if it can be
CC integrated in the canonical pathway, as PKC seems to be required
CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
CC to involve interactions with G-proteins. May be involved in
CC transduction and intercellular transmission of polarity
CC information during tissue morphogenesis and/or in differentiated

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CC tissues.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Most abundant in fetal kidney, followed by
CC brain and lung. In adult tissues, expressed in kidney, heart,
CC pancreas and skeletal muscle
CC -1- DOMAIN: Lys-THR-X-X-TIP motif is involved in the activation of
CC the Wnt/beta-catenin signaling pathway (By similarity).
CC -1- DOMAIN: The Fz domain is involved in binding with Wnt ligands (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
CC RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; AB043703; BAB41064.1; -.
CC DR EMBL; AL121748; CAC10185.1; -.
CC DR Genew; HGNC:4046; FZD8.
CC DR MIM; 606146; -.
CC DR InterPro; IPR000539; Frizzled.
CC DR InterPro; IPR000024; Fz domain.
CC DR InterPro; IPR000832; GPCR_secretin.
CC DR Pfam; PF01392; Fz; 1.
CC DR Pfam; PF01534; Frizzled; 1.
CC DR SMART; SM00063; FRI; 1.
CC DR SMART; SM00489; FRIZZLED.
CC DR PROSITE; PS50261; G-PROTEIN RECEPTOR; 1.
CC DR PROSITE; PS50038; Fz; 1.
CC KW Multigene family; G-protein coupled receptor; Transmembrane;
CC Developmental protein; Glycoprotein; Signal.
CC FT SIGNAL 1 27
CC FT CHAIN 28 694
CC FT DOMAIN 28 275 FRIZZLED 8.
CC FT TRANSMEM 276 296 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 297 312 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 313 333 2 (POTENTIAL).
CC FT DOMAIN 334 396 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 397 417 3 (POTENTIAL).
CC FT DOMAIN 418 439 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 440 460 4 (POTENTIAL).
CC FT DOMAIN 461 483 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 484 504 5 (POTENTIAL).
CC FT DOMAIN 505 532 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 533 553 6 (POTENTIAL).
CC FT DOMAIN 554 584 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 585 605 7 (POTENTIAL).
CC FT DOMAIN 606 694 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 608 694 FZ.
CC FT DOMAIN 168 172 POLY-PRO.
CC FT DOMAIN 194 202 POLY-GLY.
CC FT DOMAIN 211 216 POLY-GLY.
CC FT DOMAIN 639 663 POLY-GLY.
CC FT SITE 608 613 LYS-THR-X-X-TRP MOTIF.
CC FT SITE 692 694 PDZ-BINDING.
CC FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 694 AA; 73300 MW; E740CBFDA2A233EF CRC64;

Query Match 62.9%; Score 824; DB 1; Length 694;
Best Local Similarity 59.9%; Pred. No. 2.1e-57;
Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;

QY 11 LLLLAQLVGRRAAASKAPVCEITVPMCRGIGYVLTMPNPFNDTODEAGLEVH 68
DB 11 LLLLAQLVGRRAAASKAPVCEITVPMCRGIGYVLTMPNPFNDTODEAGLEVH 70

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QY 69 QFWPLVEICSPDLRFLCTMTPTICLPDYHKLPPCRSVCEKAKGCSPLMYQYFAMP 128
 DB 71 QFWPLVEICSPDLRFLCTMTPTICLPDYHKLPPCRSVCEKAKGCSPLMYQYFAMP 130
 QY 129 ERMSCDRLPVLGRDAEVLCDMDYRSEATTA---PPRPPAKTLPG-----PPG 174
 DB 131 DMRRCRLPEQG-NPDTLCMDYRKTDLTTAAPSPPRLPPP--PGEOPSSGSHRPPG 187
 QY 175 A-----PASG-----ECPAGGFV-----CKREPFVPLKESH 205
 DB 188 ARPHRGGGSGGGAAPAPRGGGGGKARPPGGGAACERCCGCRAMVSVSSERHP 247
 QY 206 LYNKATGVPCVPCYOPSSADERTF 234
 DB 248 LYNKATGVPCVPCYOPSSADERTF 276

RESULT 5
 FZDB_MOUSE STANDARD; PRT; 685 AA.
 ID FZDB_MOUSE STANDARD; PRT; 685 AA.
 AC Q61091;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Frizzled 8 precursor (Frizzled-8) (Fz-8) (MF28).
 GN FZDB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96224032; PubMed=8626800;
 RA Wang Y., Macke J.P., Abella B.S., Andreasson K., Worley P.,
 RA Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.,
 RT "A large family of putative transmembrane receptors homologous to the
 product of the Drosophila tissue polarity gene frizzled.";
 RL J. Biol. Chem. 271:4468-4476 (1996).
 RN (2)
 RP COUPLING TO BETA-CATENIN PATHWAY.
 RX MEDLINE=99324245; PubMed=10395542;
 RA Sheidahl L.C., Park M., Malbon C.C., Moon R.T.,
 RT "Protein kinase C is differentially stimulated by Wnt and Frizzled
 homologs in a G-protein-dependent manner.";
 RL Curr. Biol. 9:695-698 (1999).
 CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 are coupled to the beta-catenin canonical signaling pathway, which
 leads to the activation of dishevelled proteins. Inhibition of
 GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 of Wnt target genes. A second signaling pathway involving PKC and
 calcium fluxes has been seen for some family members, but it is
 not yet clear if it represents a distinct pathway or if it can be
 integrated in the canonical pathway, as PKC seems to be required
 for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 to involve interactions with G-proteins. May be involved in
 transduction and intercellular transmission of polarity
 information during tissue morphogenesis and/or in differentiated
 tissues. Activation by Wnt induces expression of beta-catenin
 target genes.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in chondrocytes.
 CC -1- DOMAIN: Lys-Thr-X-X-Tip motif is involved in the activation of
 the Wnt/beta-catenin signaling pathway (By similarity).
 CC -1- DOMAIN: The Fz domain is involved in binding with Wnt ligands (By
 similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
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 CC -----
 CC EMBL: U43371; AAC52433.1; -
 DR MGD; MGI:108460; Fzdb.
 DR InterPro; IPR000539; Frizzled.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF01392; Fz; 1.
 DR Pfam; PF01534; Frizzled; 1.
 DR PRINTS; PR00489; FRIZZLED.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PS50038; Fz; 1.
 DR PROSITE; PS50261; G-PROTEIN RECEPTOR F2.4; 1.
 DR Multigene family; G-protein coupled receptor; Transmembrane;
 KW Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1 27
 FT CHAIN 1 685
 FT DOMAIN 28 272
 FT TRANSMEM 273 293
 FT DOMAIN 294 309
 FT TRANSMEM 310 330
 FT DOMAIN 331 394
 FT TRANSMEM 395 415
 FT DOMAIN 416 437
 FT TRANSMEM 438 458
 FT DOMAIN 459 481
 FT TRANSMEM 482 502
 FT DOMAIN 503 530
 FT TRANSMEM 531 551
 FT DOMAIN 552 582
 FT TRANSMEM 583 603
 FT DOMAIN 604 685
 FT DOMAIN 30 151
 FT DOMAIN 168 173
 FT DOMAIN 353 361
 FT DOMAIN 640 654
 FT SITE 606 611
 FT SITE 683 685
 FT CARBOHYD 49 49
 FT CARBOHYD 152 152
 FT CARBOHYD 473 473
 SQ SEQUENCE 685 AA; 73215 MW; F333B49474411267 CRC64;
 Query Match 62.9%; Score 823.5; DB 1; Length 685;
 Best Local Similarity 60.0%; Pred. No. 2,3e-57;
 Matches 159; Conservative 24; Mismatches 39; Indels 43; Gaps 8;
 QY 11 SLT--LLLLAQLVGRRAAASAKAPVCOEIVPMCRGIGYVLTMPNQHNDTODEAGLEVH 68
 DB 11 SLTAAALAVIGRSSGAAMASAKELACOEIVPLCKIGVYTTMPNQHNDTODEAGLEVH 70
 QY 69 QFWPLVEICSPDLRFLCTMTPTICLPDYHKLPPCRSVCEKAKGCSPLMYQYFAMP 128
 DB 71 QFWPLVEICSPDLRFLCTMTPTICLPDYHKLPPCRSVCEKAKGCSPLMYQYFAMP 130
 QY 129 ERMSCDRLPVLGRDAEVLCDMDYRSEATTA---PPRPPAKTLPG-----PPG 174
 DB 131 DMRRCRLPEQG-NPDTLCMDYRKTDLTTAAPSPPRLPPP--PGEOPSSGSHRPPG 187
 QY 175 A-----PASG-----ECPAGGFV-----CKREPFVPLKESH 209
 DB 188 ARPHRGGGSGGGAAPAPRGGGGGKARPPGGGAACERCCGCRAMVSVSSERHP 248
 QY 210 VRTGVPCVPCYOPSSADERTF 234
 DB 249 VRTGVPCVPCYOPSSADERTF 273

RESULT 6
 FZDB_XENLA STANDARD; PRT; 581 AA.
 ID FZDB_XENLA STANDARD; PRT; 581 AA.

AC 093274; Q9Y155;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Frizzled 8 precursor (Frizzled-8) (Fz-8) (Xfz8).
 GN FZ8.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OK NCBI_TaxID=8355;
 RN (1)
 RP SEQUENCE FROM N.A., AND COUPLING TO BETA-CATENIN PATHWAY.
 RC TISSUE=embryo;
 RX PubMed=9651509;
 RA Itoh K., Jacob J., Sokol S.Y.;
 RT "A role for Xenopus Frizzled 8 in dorsal development.";
 RL Mech. Dev. 74:145-157(1998).
 RL (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=embryo;
 RX MEDLINE=98301424; PubMed=9636083;
 RA Dearforff M.A., Tan C., Conrad L.J., Klein P.S.;
 RT "Frizzled-8 is expressed in the Spemann organizer and plays a role in
 early morphogenesis.";
 RL Development 125:2687-2700(1998).
 CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 are coupled to the beta-catenin canonical signaling pathway, which
 leads to the activation of dishevelled proteins, inhibition of
 GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 of Wnt target genes. A second signaling pathway involving PKC and
 calcium fluxes has been seen for some family members, but it is
 not yet clear if it represents a distinct pathway or if it can be
 integrated in the canonical pathway, as PKC seems to be required
 for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 to involve interactions with G-proteins. May be involved in
 transduction and intercellular transmission of polarity
 information during tissue morphogenesis and/or in differentiated
 tissues. Activation by Wnt8, Wnt5A or Wnt3A induces expression of
 beta-catenin target genes. Displays an axis-inducing activity.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DEVELOPMENTAL STAGE: First expressed at high levels in the late
 blastula stages. At early gastrula, expressed in the deep cells of
 the Spemann organizer prior to involution of the dorsal blastopore
 lip. Detected in presumptive neuroectoderm as gastrulation
 proceeds. Becomes restricted to the anterior ectoderm by the end
 of gastrulation. At neurula stages, localized in the most anterior
 region of the embryo, mainly in the anterior ectoderm including
 telencephalic and cement gland regions.
 CC -1- DOMAIN: Lys-Thr-X-X-X-Tyr motif is involved in the activation of
 the Wnt/beta-catenin signaling pathway (by similarity).
 CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (by
 similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL, AF011777, AAC31121.1, -;
 DR EMBL, AF033110, AAC77361.1, -;
 DR InterPro, IPR000539, Frizzled.
 DR InterPro, IPR000024, Fz domain.
 DR InterPro, IPR000832, GPCR_secretin.
 DR Pfam, PF01392, Fz; 2.
 DR Pfam, PF01534, Frizzled; 2.
 DR PRINTS, PR00489, FRIZZLED.

DR SMART, SM00063; PRI, 1.
 DR PROSITE, PS50038; FZ, 1.
 DR PROSITE, PS50261; G PROTEIN RECEPTOR F2.4; 1.
 KM Multigene family: G-protein coupled receptor; Transmembrane;
 Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1
 FT CHAIN 24
 FT DOMAIN 24 581
 FT TRANSMEM 240 260
 FT DOMAIN 261 271
 FT TRANSMEM 272 292
 FT DOMAIN 293 320
 FT TRANSMEM 321 341
 FT DOMAIN 342 378
 FT TRANSMEM 378 398
 FT DOMAIN 399 407
 FT TRANSMEM 408 428
 FT DOMAIN 429 454
 FT TRANSMEM 455 475
 FT DOMAIN 476 505
 FT TRANSMEM 506 526
 FT DOMAIN 527 581
 FT SITE 529 534
 FT SITE 579 581
 FT CARBOHYD 42 42
 FT CARBOHYD 146 146
 FT CONFLICT 1 3
 FT CONFLICT 7 7
 FT CONFLICT 10 10
 FT CONFLICT 14 14
 FT CONFLICT 20 20
 FT CONFLICT 135 135
 FT CONFLICT 171 171
 FT CONFLICT 175 175
 FT CONFLICT 185 185
 FT CONFLICT 216 216
 FT CONFLICT 237 237
 FT CONFLICT 494 496
 FT CONFLICT 500 500
 FT CONFLICT 547 547
 FT CONFLICT 565 565
 FT CONFLICT 572 572
 SQ SEQUENCE 581 AA; 65378 MW; 80890C408AB21E23 CRC64;
 Query Match 61.2%; Score 802; DB 1; Length 581;
 Best Local Similarity 63.9%; Pred. No. 9.5e-56;
 Matches 149; Conservative 25; Mismatches 43; Indels 16; Gaps 5;
 QY 13 LLLLLAQLVGRRAAASKAVCOEITVPMCRGIGYNTLTHNPNOFNHDTODAGLEVHQFMP 72
 DB 8 LLLVSWLWGSGCAAKKELSCOEITVPLCKDIGYNTVMPNQFNHDTODAGLEVHQFMP 67
 QY 73 LVEIQSPDLRFPLCTMYTPICLPDYHKLPPCRSVCERAKGCSPLMYQYGFAMEERMS 132
 DB 68 LVVHICSPDLKFLCTMYTPICLEDYKPLPCRSVCERARAGCAPLMRYGFAMWDRMR 127
 QY 133 CDRLPLVIGDAEVLQMD-VNRSSEATT-APPRPAPV-----TLGGPPGAPASGGE 181
 DB 128 CDLPLPQGG-NPDLTCDMYNRTQTAAASHPPKPPARSPVKTRVPEPPSRRAIG 186
 QY 182 CPAGSPFVCKREPPVPLIKESHPLYNKYRTQGVNCAVCYQSPFSADERTP 234
 DB 187 CEGS-----CQCRAPMVQVSNERNRPLVNRVRTQIPIRCAMPCHNPFSPERTP 235
 RESULT 7
 FRZ2 DROME STANDARD; PRT; 694 AA.
 ID FRZ2 DROME
 AC 094916;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Frizzled protein 2 precursor (Frizzled-2) (DFZ2).
 GN FZ2 OR CG9739.
 OC Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 NC NCBI_TaxID=7227;
 RN (1)
 RP SEQUENCE FROM N.A., AND BINDING TO WINGLESS THROUGH FZ DOMAIN.
 RX MEDLINE=6535971; PubMed=8717036;
 RA Bhatnag P., Brink M., Samos C.H., Hsieh J.C., Wang Y., Macke J.P.,
 RA Andrew D., Nathans J., Nusse R.,
 RT "A new member of the frizzled family from Drosophila functions as a
 RT wingless receptor.";
 RL Nature 382:225-230(1996).
 (2)
 RN SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Bence P.V., Bernick B.P., Bhandari D., Bolshakov S.,
 RA Borovoy D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasner K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
 RA Jalali M., Kalush F., Kapten G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasbo P., Lei Y., Levytsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mouton G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Paczib J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reineert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Weissman D.A., Weissrock G.M., Weissbach J.,
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RL "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 CC are coupled to the beta-catenin canonical signaling pathway, which
 CC leads to the activation of dishevelled proteins. Inhibition of
 CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 CC of Wnt target genes. A second signaling pathway involving PKC and
 CC calcium fluxes has been seen for some family members, but it is
 CC not yet clear if it represents a distinct pathway or if it can be
 CC integrated in the canonical pathway, as PKC seems to be required
 CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 CC to involve interactions with G-proteins. Required to coordinate
 CC the cytoskeletons of epidermal cells to produce a parallel array
 CC of cuticular hairs and bristles.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -1- DEVELOPMENTAL STAGE: Expression starts at stage 6 in all cells
 CC between 15 and 70 per cent of egg length, including the
 CC invaginating cells of the ventral furrow. Stripe pattern is

emerging by early stage 8. From stage 9 and continuing throughout
 embryogenesis, expression is seen in the developing CNS. At stage
 10, expressed in 15 stripes in the presumptive head and trunk
 regions, in the posterior midgut primordium, in a subset of cells
 of anterior midgut invagination and in the procephalic lobe. At
 stage 12, expression declines in epidermis and increases in the
 midgut and visceral mesoderm. At stage 17, only expressed in the
 CNS, hindgut and dorsal vessel.
 CC -1- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of
 CC the Wnt/beta-catenin signaling pathway (By similarity).
 CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands.
 CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SWO OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
 CC -----
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 CC -----

EMBL; U65589; AAC47273.1; -
 DR EMBL; AE003518; AAF49184.1; -
 CC FLYBASE: FBgn0016797; fz2.
 DR InterPro: IPR000539; Frizzled.
 DR InterPro: IPR000024; Fz domain.
 DR InterPro: IPR000832; GPCR_secretin.
 DR Pfam: PF01534; Frizzled; I.
 DR Pfam: PF01534; Fz; 1.
 DR PRINTS: PR00489; FRIZZLED.
 DR SMART: SM00063; FRI; 1.
 DR PROSITE: PS00318; FZ; 1.
 DR PROSITE: PS00261; G-PROTEIN_RECEP_F2_4; 1.
 DR KEGG: MultiGene family; Receptor; G-protein coupled receptor; Transmembrane;
 CC KW: Developmental protein; Glycoprotein; Signal.
 FT SIGNAL. 1 22
 FT CHAIN. 23 694
 FT DOMAIN. 23 315
 FT TRANSMEM. 316 336
 FT TRANSMEM. 337 352
 FT TRANSMEM. 353 373
 FT DOMAIN. 374 397
 FT TRANSMEM. 398 418
 FT DOMAIN. 419 439
 FT TRANSMEM. 440 460
 FT DOMAIN. 461 482
 FT TRANSMEM. 483 503
 FT DOMAIN. 504 534
 FT TRANSMEM. 535 555
 FT DOMAIN. 556 584
 FT TRANSMEM. 585 605
 FT DOMAIN. 606 694
 FT DOMAIN. 187 225
 FT DOMAIN. 59 180
 FT SITE. 608 613
 FT SITE. 652 654
 FT CARBOHYD. 78 78
 FT CARBOHYD. 288 288
 FT CONFLICT. 55 55
 FT CONFLICT. 417 417
 SO SEQUENCE. 694 AA; 75451 MW; 6C310F13CAFP096 CRC64;

Query Match 47.4%; Score 621; DB 1; Length 694;
 Best Local Similarity 43.4%; Pred. No. 1.6e-41;
 Matches 124; Conservative 27; Mismatches 55; Indels 80; Gaps 7;

QY 22 GRAAASKP-----VCOEITVPMCGIGVNLTHMPNCFNPDODAGLEVA 68
 DB 40 GAGLDASPAAGVGVPIPDNLRCEIITVPMCRGIGVNMTPSPNMEHTODAGLEVA 99
 QY 69 QFWPLVEIQCSPDLRFPLCTMYTPICLPDYHKPLPGRSVCCERAKAGCSPLMKROYFAMP 128

[illegible]

FT	DOMAIN	306	332	353	EXTRECELLULAR (POTENTIAL)
FT	TRANSMEM	333	353	333	3 (POTENTIAL)
FT	DOMAIN	354	375	375	CYTOPLASMIC (POTENTIAL)
FT	TRANSMEM	376	396	396	4 (POTENTIAL)
FT	DOMAIN	397	419	419	EXTRACELLULAR (POTENTIAL)
FT	TRANSMEM	420	440	440	5 (POTENTIAL)
FT	DOMAIN	441	466	466	CYTOPLASMIC (POTENTIAL)
FT	TRANSMEM	467	487	487	6 (POTENTIAL)
FT	DOMAIN	488	524	524	EXTRACELLULAR (POTENTIAL)
FT	TRANSMEM	525	545	545	7 (POTENTIAL)
FT	DOMAIN	546	570	570	CYTOPLASMIC (POTENTIAL)
FT	DOMAIN	39	158	158	PZ.
FT	DOMAIN	186	192	192	LYS-THR-X-X-TRP MOTIF.
FT	SITE	548	553	553	PDZ-BINDING.
FT	SITE	568	570	570	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	58	58	58	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	159	159	159	N-LINKED (GLCNAC. . .) (POTENTIAL)
SEQ	SEQUENCE	570 AA;	63885 MW;	4FB895D9BEAFCA4E CRC64;	
Query Match		35.6%;	Score 466;	DB 1;	Length 570;
Best Local Similarity		41.1%;	Pred. No. 1.8e-25;		
Matches 106;	Conservative	30;	Mismatches 84;	Indels 38;	Gaps 10;
Qy	2	ARPDSPAPRSLLLLLLAQVGRRAAASAKAPV-----COEITVPMCRGIGNYLTMPNQ	54		
Db	6	ALPNSALPRLLILLPLLLPLPRAQPHGKSGISIPHGSCQPSITFLCTDIAYNOTIMNL	65		
Qy	55	FNHDTQDAGLEVHQFWELVEIQCSFPLRFLCTWYTRICLPDYHKKPLRPCRVCERAKA	114		
Db	66	LIGHTQEDAGLEVHQFYLVKVCSPELRFLCWSMYAIVCTV-LEQAIIPCRSICERARO	124		
Qy	115	GCSELMQCYGAWPERPNSCDRLVIGRAEVLCDMDYNSE-----ATTAPRPPAPKPT	168		
Db	125	GCEALMKNFGQWPERPLRCEHFPRHG--AEQICVQGNSEEGTPLLTTAPSGI--QPG	180		
Qy	169	LRPGPAPASGEGECAGS-----PFWCKCREPFPVLPIKESHPLYNKVRTGQVNCAPCYO	224		
Db	181	AGGTPGGFGGCGAPPRVYTLTHPRHCP-----RVLKV--PSYLSYKFLGERDCAAPC-E	231		
Qy	225	PS-----FSADERTPA	235		
Db	232	PARPGSMFESHHTRFA	249		
RESULT 11					
FZD7 HUMAN					
ID	FZD7 HUMAN	STANDARD;	PRT;	574 AA.	
AC	075084; 094816;				
DT	15-JUN-2002 (Rel. 41, Created)				
DT	15-JUN-2002 (Rel. 41, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Frizzled 7 precursor (Frizzled-7) (Fz7) (FZB3).				
GN	FZD7.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND COUPLING TO BETA-CATENIN PATHWAY.				
RC	TISUSeOesophageal carcinoma;				
RC	MEDLINE=98374323; PubMed=9707618;				
RA	Tanaka S., Akiyoshi T., Mori M., Wands J.R., Sugimachi K.;				
RT	"A novel frizzled gene identified in human esophageal carcinoma				
RT	mediates APC/beta-catenin signals."				
RL	Proc. Natl. Acad. Sci. U.S.A. 95:10164-10169(1998).				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISUSeFetal lung;				
RC	MEDLINE=99032814; PubMed=9813155;				
RA	Sagara N., Toda G., Hirai M., Terada M., Katoh M.;				
RT	"Molecular cloning, differential expression, and chromosomal				
RT	localization of human frizzled-1, frizzled-2, and frizzled-7,"				
RL	Biochem. Biophys. Res. Commun. 252:117-122(1998).				

CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 CC are coupled to the beta-catenin canonical signaling pathway, which
 CC leads to the activation of dishevelled proteins, inhibition of
 CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 CC of Wnt target genes. A second signaling pathway involving PKC and
 CC calcium fluxes has been seen for some family members, but it is
 CC not yet clear if it represents a distinct pathway or if it can be
 CC integrated in the canonical pathway, as PKC seems to be required
 CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 CC to involve interactions with G-proteins. May be involved in
 CC transduction and intercellular transmission of polarity
 CC information during tissue morphogenesis and/or in differentiated
 CC tissues.
 CC SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: High expression in adult skeletal muscle and
 CC fetal kidney, followed by fetal lung, adult heart, brain, and
 CC placenta. Specifically expressed in squamous cell esophageal
 CC carcinoma.
 CC -1- DOMAIN: Lys-Thr-X-X-X-Tyr motif is involved in the activation of
 CC the Wnt/beta-catenin signaling pathway (By similarity).
 CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
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 CC -----
 CC EMBL: AB010881; BAA3424.1; -
 CC EMBL: AB017365; BAA34668.1; -
 CC Genew; HGNC:4045; FZD7.
 CC DR MIM: 603410; -
 CC DR InterPro: IPR000539; Frizzled.
 CC DR InterPro: IPR000024; Fz domain.
 CC DR InterPro: IPR000832; GPCR_secretin.
 CC DR Pfam: PF01392; Fz; 1.
 CC DR Pfam: PF01534; Frizzled; 1.
 CC DR PRINTS: PR00489; FRIZZLED.
 CC DR SMART: SM00063; FRI; 1.
 CC DR PROSITE: PS50038; FZ; 1.
 CC DR PROSITE: PS50261; G-PROTEIN COUPLED RECEPTOR; Transmembrane;
 CC Multigene family; G-protein coupled receptor; Transmembrane;
 CC Developmental protein; Glycoprotein; Signal.
 CC KW SIGNAL 1
 CC FT CHAIN 1 574
 CC FT DOMAIN 33 256
 CC FT TRANSMEM 257 277
 CC FT DOMAIN 278 288
 CC FT TRANSMEM 289 309
 CC FT DOMAIN 310 336
 CC FT TRANSMEM 337 357
 CC FT DOMAIN 358 379
 CC FT TRANSMEM 380 400
 CC FT DOMAIN 401 423
 CC FT TRANSMEM 424 444
 CC FT DOMAIN 445 470
 CC FT TRANSMEM 471 491
 CC FT DOMAIN 492 528
 CC FT TRANSMEM 529 549
 CC FT DOMAIN 550 574
 CC FT TRANSMEM 574 594
 CC FT DOMAIN 595 615
 CC FT TRANSMEM 616 636
 CC FT SITE 552 557
 CC FT SITE 572 574
 CC FT CARBOHYD 63 63
 CC FT CARBOHYD 164 164
 CC FT CONFLICT 8 8
 CC FT CONFLICT 15 15
 CC F -> L (IN REF. 2).
 CC F -> L (IN REF. 2).

FT CONFLICT 201 201 K -> R (IN REF. 2).
 FT CONFLICT 308 308 F -> L (IN REF. 2).
 FT CONFLICT 408 408 N -> S (IN REF. 2).
 FT CONFLICT 415 415 F -> L (IN REF. 2).
 FT CONFLICT 433 433 F -> L (IN REF. 2).
 FT CONFLICT 447 447 F -> L (IN REF. 2).
 FT CONFLICT 534 534 C -> Y (IN REF. 2).
 SQ SEQUENCE 574 AA; 63757 MW; BB868B9C2CFBD42 CRC64;
 Query Match 34.9%; Score 457; DB 1; Length 574;
 Best Local Similarity 39.7%; Pred. No. 98-29; Indels 46; Gaps 12;
 Matches 106; Conservative 34; Mismatches 81;
 QY 1 MARPPSAPPSTL---LTLAQLVGRRAAASRAP-----VCQBITVPKCRGI 44
 DB 1 MNDPGAAYVLSLGFCAVLIALGLASAGAPHYNGKGISVPHGFCQPSISPLCTDI 60
 QY 45 GYNLTMPNQFNHDTQDEAGLEVQFWPLVEIQCSFDLFFLCTMYTPICLPDYHKPLPP 104
 DB 61 AVNQTLLPMLHQTQDEAGLEVQFWPLVVKVQCSFELFFLSMYAPVCTV-LDQAI 119
 QY 105 CRSVCERAKAGSPLMROYGFAMPERMSCDRLPYIGRDAEVLQMDVNRSEATTAP--PR 161
 DB 120 CSRSLGRARQGEALMNKFGFQWPERKRCENPVRHG--AGEICVGNITDGGSGGPGCGFT 177
 QY 162 PPAKFTLPG-----PPGAPASGCECPAGCPVCKREPPYILKESHPLYNKYRTGV 215
 DB 178 AVPTAPVLPDLFTPLPFG--ASDCKGRAPFPSC-RQLKXP-----PYIGYRTLGE- 227
 QY 216 PNCVAIPCQPS-----FSADERTFA 235
 DB 228 RDCGAPC-EPGRANGIMYFKEERERFA 253

RESULT 12
 FZD7_MOUSE
 ID FZD7_MOUSE STANDARD; PRT; 572 AA.
 AC 061090;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Frizzled 7 precursor (Frizzled-7) (Fz-7) (m277).
 GN FZD7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OK NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96224032; PubMed=8626800;
 RA Wang Y., Macke J.P., Abella B.S., Andreasson K., Worley P.,
 RA Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.,
 RA "A large family of putative transmembrane receptors homologous to the
 RA product of the Drosophila tissue polarity gene frizzled.";
 RN J. Biol. Chem. 271:4468-4476(1996).
 RP [2]
 RP COUPLING TO BETA-CATENIN PATHWAY.
 RX MEDLINE=99324245; PubMed=10395542;
 RA Sheidahl L.C., Park M., Malbon C.C., Moon R.T.;
 RA "Protein kinase C is differentially stimulated by Wnt and Frizzled
 RA homologs in a G-protein-dependent manner.";
 RL Curr. Biol. 9:695-698(1999).
 CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 CC are coupled to the beta-catenin canonical signaling pathway, which
 CC leads to the activation of dishevelled proteins, inhibition of
 CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 CC of Wnt target genes. A second signaling pathway involving PKC and
 CC calcium fluxes has been seen for some family members, but it is
 CC not yet clear if it represents a distinct pathway or if it can be
 CC integrated in the canonical pathway, as PKC seems to be required
 CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 CC to involve interactions with G-proteins. May be involved in
 CC transduction and intercellular transmission of polarity

CC information during tissue morphogenesis and/or in differentiated
 CC tissues. Activation by Wnt8 induces expression of beta-catenin
 CC target genes.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: Lys-Thr-X-X-Tyr motif is involved in the activation of
 CC the Wnt/beta-catenin signaling pathway (By similarity).
 CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
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 CC -----
 CC EMBL: U43320; AAC52432.1; -
 CC MGD: MGI:108570; Fzd7.
 CC InterPro: IPR000539; Frizzled.
 CC InterPro: IPR000024; Fz_domain.
 CC InterPro: IPR000832; GPCR_secretin.
 CC Pfam: PF01392; Fz_1.
 CC Pfam: PF01334; Frizzled; 1.
 CC PRINTS: PRO00489; FRIZZLED.
 CC SMART: SM00063; FRI; 1.
 CC PROSITE: PS50038; FZ; 1.
 CC PROSITE: PS50261; G-PROTEIN RECEPTOR_F2_4; 1.
 CC KMW: Multigene family; G-protein coupled receptor; Transmembrane;
 CC Developmental protein; Glycoprotein; Signal.
 CC SIGNAL: 1 32
 CC CHAIN: 33 572
 CC FT DOMAIN: 33 254
 CC FT TRANSMEM: 255 275
 CC FT DOMAIN: 276 286
 CC FT TRANSMEM: 287 307
 CC FT DOMAIN: 308 334
 CC FT TRANSMEM: 335 355
 CC FT DOMAIN: 356 377
 CC FT TRANSMEM: 378 398
 CC FT DOMAIN: 399 421
 CC FT TRANSMEM: 422 442
 CC FT DOMAIN: 443 468
 CC FT TRANSMEM: 469 489
 CC FT TRANSMEM: 490 526
 CC FT TRANSMEM: 527 547
 CC FT DOMAIN: 548 572
 CC FT DOMAIN: 573 633
 CC FT SITE: 550 555
 CC FT SITE: 570 572
 CC FT CARBOHYD: 63 63
 CC FT CARBOHYD: 164 164
 CC SQ SEQUENCE: 572 AA; 63816 MW; 35A68079AC786DF5 CRC64;
 CC -----
 CC Query Match 33.6%; Score 440.5; DB 1; Length 572;
 CC Best Local Similarity 38.8%; Pred. No. 1.7e-27;
 CC Matches 100; Conservative 36; Mismatches 75; Indels 47; Gaps 12;

QY 171 GPGAPASGCECPAG-----PFVCKREPFVPLIKESHPLYNKRVGTQVNCVPCYQ 224
 DB 187 DPPTFAMS-----PSDCGRSLSPFSCP-RQLKVP-----PLYGRFLGE-RDCGAPC-E 233
 QY 225 PS-----FSADERTFA 235
 DB 234 PGRANGLMYKEERERFA 251
 RESULT 13
 ID FZD2_XENLA STANDARD; PRT; 551 AA.
 AC Q9P0U6;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Frizzled 2 precursor (Frizzled-2) (Fz-2) (Xfz2).
 GN FZ2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head;
 RX MEDLINE=99425192; PubMed=10495293;
 RA Deardorff M.A., Klein P.S.;
 RT "Xenopus frizzled-2 is expressed highly in the developing eye, otic
 RT vesicle and somites."
 RL Mech. Dev. 87:229-233 (1999).
 CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 CC are coupled to the beta-catenin canonical signaling pathway, which
 CC leads to the activation of dishevelled proteins. Inhibition of
 CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 CC of Wnt target genes. A second signaling pathway involving PKC and
 CC calcium fluxes has been seen for some family members, but it is
 CC not yet clear if it represents a distinct pathway or if it can be
 CC integrated in the canonical pathway, as PKC seems to be required
 CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 CC to involve interactions with G-proteins. May be involved in
 CC transduction and intercellular transmission of polarity
 CC information during tissue morphogenesis and/or in differentiated
 CC tissues.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed, especially in the eye
 CC anlage, otic vesicle and developing somites.
 CC -1- DEVELOPMENTAL STAGE: Minimal expression in oocytes and embryos
 CC prior to mid-blastula transition. Readily detected in the
 CC presumptive tissue from late gastrulae. By neurula stages, somitic
 CC expression is broader and also appears in developing neural
 CC structures and other anterior structures (eye anlage). By late
 CC neurula, the posterior expression is condensed into two stripes on
 CC each side, expression in the anterior tissues remains high in the
 CC developing eye. During tailbud stages, expression is still high in
 CC the eye vesicle, otic vesicle and other anterior regions, as well
 CC as the presumptive mesoderm. In the tadpole, highly expressed in
 CC the head, eye and otic vesicle, branchial arches and midportion of
 CC the somites.
 CC -1- DOMAIN: Lys-Thr-X-X-Tyr motif is involved in the activation of
 CC the Wnt/beta-catenin signaling pathway (By similarity).
 CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
 CC -----
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CC -----
CC EMBL: AF139165; AAF06359.1; -
CC InterPro: IPR000539; Frizzled.
CC InterPro: IPR000024; Fz domain.
CC InterPro: IPR000832; GPCR_secretin.
CC Pfam: PF01392; Fz; 1.
CC Pfam: PF01394; Frizzled; 1.
CC PRINTS: PR00469; FRIZZLED.
CC SMART: SM00063; FRI; 1.
CC PROSITE: PS50038; Fz; 1.
CC PROSITE: PS50261; G-PROTEIN COUPLED RECEPTOR; Transmembrane;
CC Multigene family; G-protein coupled receptor; Transmembrane;
CC Developmental protein; Glycoprotein; Signal.
CC SIGNAL 1
CC CHAIN 27 551 FRIZZLED 2.
CC DOMAIN 27 231 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 232 252 1 (POTENTIAL).
CC TRANSMEM 253 265 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 266 286 2 (POTENTIAL).
CC TRANSMEM 287 313 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 314 334 3 (POTENTIAL).
CC DOMAIN 335 356 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 357 376 4 (POTENTIAL).
CC DOMAIN 378 400 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 401 421 5 (POTENTIAL).
CC TRANSMEM 422 447 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 448 468 6 (POTENTIAL).
CC TRANSMEM 469 505 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 506 526 7 (POTENTIAL).
CC TRANSMEM 529 534 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 535 552 FZ.
CC DOMAIN 533 152 LYS-THR-X-X-X-TRP MOTIF.
CC SITE 529 534 PDZ-BINDING.
CC SITE 549 551 PDZ-BINDING.
CC CAROXYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CAROXYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 551 AA: 62461 MW: 3F29F168B8E6E07 CRC64;

Query Match 33.5%; Score 438.5; DB 1; Length 551;
Beet Local Similarity 41.6%; Pred. No. 2.4e-27;
Matches 99; Conservative 29; Mismatches 73; Indels 37; Gaps 10;

QY 12 LLLLLLQVVG-RAAASAPVCOEITVPMCRGIGNLTHMNOHDTQDAGLEVHQF 70
DB 16 LPTLSIGQLHGKSGISVPHGFCOPISIPICTDIAVNGTIMPLTLGHTQDAGLEVHQF 75
QY 71 WFLVLEQCSPLDRFELCTMTPTICLDYHKPLPRGSGVGERAKAGSPLMRQGFAMPER 130
DB 76 YFLVAVQCSSELRFLFCSTMAIPVCTV-LEQALPCCRSCICERAHGGEALMNNKGFQWPER 134
QY 131 MSCDRLPVLGRDAEVLQMDYNRSE-----ATTAPRPAPAKPTLLGPPGAPASGECPA 184
DB 135 LACENRPRRG--AEQICVQONHSEDEGPTLLTSPH-----HGTCGPPI---YATL 181
QY 185 GGPVCKREPPVPIIKESHPLYNKVRTOQVNCAPVCQPS-----PSADERTFA 235
DB 182 DHPFHCP-----RVLKV--PSLYNRFLEGKCAAPC-EPTKSDGFMEFSQGEIRFA 230

RESULT 14
FZD1_CHICK STANDARD; PRT; 592 AA.
AC 057328; Q91A07;
DR 15-JUN-2002 (Rel. 41, Created)
DR 15-JUN-2002 (Rel. 41, Last sequence update)
DR 15-JUN-2002 (Rel. 41, Last annotation update)
DE Frizzled 1 precursor (Frizzled-1) (Fz-1) (cfz-1).
GN FZD1 OR FZ1.
OS Gallus gallus (Chicken).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC Gallus.
CC NCBI_TaxId=9031;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=limb bud;
RA MEDLINE=98260739; PubMed=9598377;
RT Kengaku M., Twombly V., Tabin C.;
RT "Expression of wnt and frizzled genes during chick limb bud
RT development.";
RT Cold Spring Harb. Symp. Quant. Biol. 62:421-429(1997).
RN [2]
RP SEQUENCE OF 307-592 FROM N.A.
RX MEDLINE=20245319; PubMed=10781956;
RT Stark M.R., Biggs J.J., Schoenwolf G.C., Rao M.S.;
RT "Characterization of avian frizzled genes in cranial placode
RT development.";
RT Mech. Dev. 93:195-200(2000).
RN [3]
RP FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
are coupled to the beta-catenin canonical signaling pathway, which
leads to the activation of dishevelled proteins, inhibition of
GSK-3 kinase, nuclear accumulation of beta-catenin and activation
of Wnt target genes. A second signaling pathway involving PKC and
calcium fluxes has been seen for some family members, but it is
not yet clear if it represents a distinct pathway or if it can be
integrated in the canonical pathway, as PKC seems to be required
for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
to involve interactions with G-proteins. May be involved in
transduction and intercellular transmission of polarity
information during tissue morphogenesis and/or in differentiated
tissues.
RN [4]
RP SUBCELLULAR LOCATION: Integral membrane protein.
RN [5]
RP TISSUE SPECIFICITY: Expressed in the lens, otic placode (medial
wall of the vesicle) and in epibranchial placode. Also expressed
in the developing somites (dermyotome).
RN [6]
RP DEVELOPMENTAL STAGE: Somites and placodal expression appears at
stage 9. At this stage, more obvious expression is detected in the
neural tube (midbrain and rostral hindbrain), and persists through
about stage 15. Strongly expressed in the ectoderm and around the
otic placodes at stage 12. At stage 16, otic expression declines,
expression in epibranchial placodes begins and peaks at stage 20.
Expression in the lens of the eye is first seen at about stage 15,
more evident at stage 16. At stage 17, seen in the ectoderm and
mesenchyme of the limb primordia. Detected at stage 20 in the lip
of the optic cup, in the mesenchyme surrounding the eye, in the
ectoderm overlying the lens and in the ectoderm caudal and ventral
of the olfactory placodes. From stages 20-30, expressed in
catilage and in the dermyotomes and migrating scleromal cells
forming vertebrae.
RN [7]
RP DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of
the Wnt/beta-catenin signaling pathway (By similarity).
RN [8]
RP -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
similarity).
RN [9]
RP -1- SIMILARITY: BELONGS TO FAMILY FZ/SWO OF G-PROTEIN COUPLED
RECEPTORS.
RN [10]
RP -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
RN [11]
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CC or send an email to license@1sb-sib.ch).
RN [12]
RP EMBL: AF031830; AAB87968.1; -
RN [13]
RP EMBL: AF224314; AAF61094.1; -
RN [14]
RP InterPro: IPR000539; Frizzled.
RN [15]
RP InterPro: IPR000024; Fz domain.
RN [16]
RP InterPro: IPR000832; GPCR_secretin.
RN [17]
RP Pfam: PF01392; Fz; 1.
RN [18]
RP Pfam: PF01534; Frizzled; 2.
RN [19]
RP PRINTS: PR00469; FRIZZLED.
RN [20]
RP SMART: SM00063; FRI; 1.
RN [21]
RP PROSITE: PS50038; Fz; 1.
RN [22]
RP PROSITE: PS50261; G-PROTEIN RECEPTOR_FZ_4; 1.

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FT	CONFLICT	352	352	S -> F (IN REF. 2).
SQ	SEQUENCE	642 AA;	70955 MW;	0AAD0C0DC820B6CE CRC64;

SO SEQUENCE 642 AA; 70955 MW; 0AAD0C0DC820B6CE CRC64;

Query Match	32.2%	Score 422;	DB 1;	Length 642,
Best local similarity	36.0%	Pred NO 5	4e-26.	

Matches 102; Conservative 32; Mismatches 87; Indels 62; Gaps 10;

Matches 102; Conservative 32; Mismatches 87; Indels 62; Gaps 10;

Qy 3 RPDGAPPSLLLL- - - - - AQLGRRAA - ASKAP - - - - - 31

Db 44 RADPRRMASSGLLLMLLEAPLLLLGLVRRQAAGVSGPQQQAPPPQQSQSQYNBGRG 103

Qy 32 - - - - - VQGEITVPMCRGIGINLTHMNPQNFHDQDEAGLEVFQFWPLVEIQSPDLRF 85

Db 104 SIPDHGYQCPISIPLCITMANMOTIMPTLLGHTNOEDAGLEVFQFWPLVKQCSAEIKFF 163

Qy 86 LCTMTPTICLPDYHNPFLPPCRSVCERAAAGCSPLMRQYGFAMPBMSCDRLPYVGRDAEV 143

Db 164 LCSMNAFPCYV - LBAALFPCCSLCERAAQSGEALMNKFGFMPTLCKEKPVHG - AGE 2220

Qy 146 LCMIDNRSEATTAPRPPAPKPTLLGPPGADASGGECPAG - - - - - GPVCKCEPVP 199

Db 221 LCVGQNTSDKGPPTPSLLPEFWTSGQHGGGGYRGVGGAGTVERGKFSCP - RALRPS 279

Qy 200 LKESHPLYNKRVQGVPCAVCPQPS - - - - - FSADERTFA 235

Db 280 YLNIHFLEK - - - - - DCGAPC - EPTNYVGLMTFGPEELRFS 314

Db 44 RADPRWASGLLLLLWLLEAPLLLGVRAGAAAGVSGPGQQA PPPPQQSGQQYNGERGI 103

32 -----VCOEITVPMCRGIGYNLTHMPNQFNHDTQDEAGLEVHOFWEIVEIQCSPLRFF 85

Db 104 SIPDHGYCQPIISIP LCTDMAYNOTIMP NLLGHTNOEDAGLEVHQFYPLVKVQCSAE LKFF 163

86 LCTMYTPICLPDYHKELPPCRSVCEERAKAGCSPLMROYGFAMPERNSCDRLPVLGRDAEV 145

164 1CSWA BYCTU-1 EOAL PBCTSI CEBAPOCCEAI MUKCEOWBDNTI KCEKEBDTUC -- JCE 320

220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

146 LCMIDINKSEATIAERPRFPAKPTLPGPGAPASGCECPAG-----GPFVCKCREPEVPI 199

Db 221 LCVGQNTSDKGTPTPSLLPEFWTSNGQHGGSYRGYPGAGTVERKXFS^{CP}-RALRVPS 279

QY 200 LKESHPYLNKVRTGQVPCNCAPCYQPS-----FSADERTFA 235

Search completed: May 19, 2003, 16:34:31
Job time : 16 secs

Job time : 16 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 19, 2003, 16:33:07 ; Search time 33 Seconds
(without alignments)
1467.305 Million cell updates/sec

Title: US-09-847-102a-68

Perfect score: 1310
Sequence: 1 MARPPSAPSLILLIAQL.....PNCAPVCQPSFSADERTFA 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	801	61.1	579	13 Q9Y100	Q9Y100 brachydanio
2	801	61.1	579	13 Q9W6E4	Q9W6E4 brachydanio
3	800	61.1	579	13 Q9PTT7	Q9PTT7 brachydanio
4	796	60.8	592	13 Q9W6E2	Q9W6E2 brachydanio
5	794	60.6	576	13 Q9Y149	Q9Y149 brachydanio
6	794	60.6	576	13 Q9PWK6	Q9PWK6 brachydanio
7	794	60.6	576	13 Q9PMN8	Q9PMN8 brachydanio
8	461	35.2	574	4 Q96B74	Q96B74 homo sapien
9	451	34.4	550	5 Q9UB06	Q9UB06 caenorhabdi
10	429.5	32.8	550	5 Q9Y117	Q9Y117 brachydanio
11	426	32.5	872	5 Q9N145	Q9N145 ciona intes
12	410.5	31.3	559	13 Q90ZT3	Q90ZT3 brachydanio
13	408.5	31.2	559	13 Q98S12	Q98S12 brachydanio
14	403	30.8	557	13 Q8QFM3	Q8QFM3 brachydanio
15	401.5	30.6	591	4 Q8TAN2	Q8TAN2 homo sapien
16	380.5	29.0	577	13 Q918V7	Q918V7 brachydanio

17	379	28.9	315	13 Q91A95	Q91A95 gallus gall
18	367.5	28.1	319	13 P79993	P79993 xenopus lae
19	367	28.0	323	11 Q91W58	Q91W58 mus musculus
20	366.5	28.0	511	5 Q95X97	Q95X97 caenorhabdi
21	366.5	28.0	539	5 Q95X96	Q95X96 caenorhabdi
22	366.5	28.0	580	13 Q9PTT8	Q9PTT8 brachydanio
23	366.5	28.0	580	13 Q9W6E3	Q9W6E3 brachydanio
24	366.5	28.0	580	13 Q90WM3	Q90WM3 brachydanio
25	360	27.5	318	13 P79936	P79936 xenopus lae
26	359.5	27.4	315	13 Q9W6E0	Q9W6E0 brachydanio
27	347.5	26.5	348	11 Q35222	Q35222 rattus norv
28	347.5	26.5	351	11 Q9Z1N6	Q9Z1N6 mus musculus
29	340.5	26.0	303	11 Q924N2	Q924N2 rattus norv
30	339.5	25.9	148	11 Q91ZX9	Q91ZX9 mus musculus
31	339.5	25.9	568	5 Q91477	Q91477 caenorhabdi
32	338.5	25.8	346	4 Q14877	Q14877 homo sapien
33	338.5	25.8	348	11 Q9JLS5	Q9JLS5 rattus norv
34	326	24.9	197	11 Q9ULS4	Q9ULS4 rattus norv
35	322	24.6	213	13 Q9PTD9	Q9PTD9 gallus gall
36	320	24.4	545	5 Q9U322	Q9U322 hydra atten
37	317	24.2	130	6 Q95J81	Q95J81 oryctolagus
38	308	23.5	537	4 Q8TAV8	Q8TAV8 homo sapien
39	293	22.4	138	13 Q9PTN5	Q9PTN5 gallus gall
40	288.5	22.0	920	5 Q9SEF3	Q9SEF3 strongyloce
41	283.5	21.6	292	13 Q91A96	Q91A96 gallus gall
42	282	21.5	704	4 Q8WXR9	Q8WXR9 homo sapien
43	279	21.3	295	11 Q9WU66	Q9WU66 mus musculus
44	278.5	21.3	295	11 Q35297	Q35297 mus musculus
45	278.5	21.3	295	11 P97299	P97299 mus musculus

ALIGNMENTS

RESULT 1	
Q9Y100	PRELIMINARY; PRT; 579 AA.
ID Q9Y100;	
AC Q9Y100;	
DT 01-MAY-1999 (TREMBLrel. 10, Created)	
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)	
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE Frizzled 8a protein.	
GN FZ8A.	
OS Brachydanio rerio (zebrafish) (zebra danio).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;	
OC Cyprinidae; Danio.	
OK NCBI_TaxID=7955;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=OREGON;	
RX MEDLINE=99077702; PubMed=9858730;	
RA Kim S.H., Park H.C., Yeo S.Y., Hong S.K., Choi J.W., Kim C.H.,	
RA Weinstein B.M., Huh T.L.;	
RT "Characterization of two frizzled homologues expressed in the	
RT embryonic shield and prechordal plate of zebrafish embryos";	
RL Mech. Dev. 78:193-201(1998).	
DR EMBL: AF060697; AAD05435.1; -	
DR ZFIN; ZDB-GENE-000328-3; fZ8a.	
DR InterPro; IPR000539; Frizzled.	
DR InterPro; IPR000024; Fz domain.	
DR InterPro; IPR000832; GPCR secretin.	
DR Pfam; PF01534; Frizzled; I.	
DR Pfam; PF01392; Fz; 1.	
DR PRINTS; PRO0469; FRIZZLED.	
DR SMART; SM00063; FRI; 1.	
DR PROSITE; PSS0038; Fz; 1.	
DR PROSITE; PSS0261; G_PROTEIN_RECPT_F2_4; 1.	
SQ SEQUENCE 579 AA; 65249 MW; AFSACG626A4EC06 CXC64;	
Query Match	61.1%; Score 801; DB 13; Length 579;
Best Local Similarity	63.1%; Pred. No. 3e-69;
Matches 147; Conservative 25; Mismatches 45; Indels 16; Gaps 6;	

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QY 13 LLLLLLQVGRRAAASKAPVCOEITVPMCRGIGYNLTMPNPFNHDTODEAGLEVHOFWP 72
DB 10 LFLALALPRSSGTTAKETTCQELAVPLCKGIGYNTYMPNPFNHDTODEAGLEVHOFWP 69
QY 73 LVEIQSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCEERAKAGCSPLMRQYGFAMPBRMS 132
DB 70 LVEIQSPDLRFPLCTMYTPICLPDYHKPLPPCRSVCEERAKAGCSPLMRQYGFAMPBRMR 129
QY 133 CDRLPVLRDAEVLQMDYNSEATAP---RP--FPAKPTLP-----GPPG-APASGGE 181
DB 130 CDLLPVQGA-PDITLQMDYNRTDSTTVSPVLSKPTNPSKAINPHKKSGRGVGPNNKMP 188
QY 182 CPAGGFVCKCRPEFVILKESHPLYNKRTGVNCAVPCYQPSFSADERTF 234
DB 189 CERG-----CQCRAWVNVSDRHLPLNRYKVGQIPNCAMPCHNPFYTOBERTF 237

RESULT 2
Q9W6E4 PRELIMINARY; PRT; 579 AA.
AC 09W6E4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
DE Frizzled protein.
GN FZ5.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN 1)
SEQUENCE FROM N.A.
RA Furutani-Seiki M.;
RT "Cloning and functional analysis of zebrafish frizzled genes.";
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF117389; AAD25359.1; -.
DR InterPro; IPR000539; Frizzled.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF01534; Frizzled; 1.
DR PRINTS; PR00489; FRIZZLED.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
SQ SEQUENCE 579 AA; 65299 MW; 6388F61A2EC8C192 CRC64;

Query Match 61.1%; Score 801; DB 13; Length 579;
Best Local Similarity 63.1%; Pred. No. 3e-69;
Matches 147; Conservative 25; Mismatches 45; Indels 16; Gaps 6;

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AC 09PTT7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
DE Frizzled homolog.
GN FZC OR ZFZC.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN 1)
SEQUENCE FROM N.A.
RA Hyatt T.M., Walsh E.E., Gutman J.R., Ekker S.C.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF039412; AAF21645.1; -.
DR ZFIN; ZDB-GENE-000210-30; fzc.
DR InterPro; IPR000539; Frizzled.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF01534; Frizzled; 1.
DR Pfam; PF01392; Fz; 1.
DR PRINTS; PR00489; FRIZZLED.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
SQ SEQUENCE 579 AA; 65265 MW; 5E84372126A4EA20 CRC64;

Query Match 61.1%; Score 800; DB 13; Length 579;
Best Local Similarity 63.1%; Pred. No. 3.7e-69;
Matches 147; Conservative 24; Mismatches 46; Indels 16; Gaps 6;

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DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE Frizzled protein.
 GN FZ6.
 OS Brachydanio rerio (zebrafish) (Zebra danio).
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Furutani-Seiki M.;
 RT "Cloning and functional analysis of zebrafish frizzled genes."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF117390; AAD25360.1; -
 DR InterPro; IPR000539; Frizzled.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR000832; GPCR secretin.
 DR Pfam; PF01534; Frizzled; 1.
 DR PRINTS; PR00489; FRIZZLED.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PS50038; FZ; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECPT_F2_4; 1.
 SQ SEQUENCE 576 AA; 64940 MW; F57E75B18629B9B6 CRC64;

Query Match 60.6%; Score 794; DB 13; Length 576;
 Best local similarity 63.5%; Pred. No. 1.4e-68;
 Matches 148; Conservative 22; Mismatches 47; Indels 16; Gaps 4;

QY 7 SAPPSSLLLLLAQLVGRAAAASAPVCOEITVPMCRGIGYNTLTMNQFNHDTODEAGLE*66
 DB 11 SALALCVLLIMSSVCGR-----EHVCOEISVPLCRGIGYNTYMPNQFNHNDQDEAGLE 64
 QY 67 VHOFPVLEIQCSPPDLRFELCTMYTPICLPDYHKPLPPCRSVCEERAAAGSPILMROYGFA 126
 DB 65 VHOFPVLEIQCSPPDLRFELCTMYTPICLPDYHKPLPPCRSVCEERAAAGSPILMROYGFP 124
 QY 127 WPERMSCDRLPVLGRDAEVLQMDYNRSEATTAPRP---FPAKPTLPFGPGAPASGSEC 182
 DB 125 WPERMCDLPLVQGG-DPNTLCMDYNRTDAISSPAAPKRTSRPGKPFKRXKSSGSSSCE 183
 QY 183 PAGPFPVCKREPPVPLKESHPLYNKVRGQVPCAVPCYQSGFSADERTFA 235
 DB 184 PE-----CYCRAPVWPVSHDHPHLYNKKVKGQIPNCAMPCHNPYLSQERTFA 231
 RESULT 8
 ID Q96B74 PRELIMINARY; PRT; 574 AA.
 AC Q96B74;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
 DE Frizzled (Drosophila) homolog 7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Strausberg R.;
 RL EMBL; BC015915; AAH15915.1; -
 DR EMBL; BC015915; AAH15915.1; -
 DR InterPro; IPR002086; Aldehyde dehydr.
 DR InterPro; IPR000539; Frizzled.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR000832; GPCR secretin.
 DR Pfam; PF01534; Frizzled; 1.
 DR Pfam; PF01392; Fz; 1.
 DR PROSITE; PS50070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
 DR PROSITE; PS50038; FZ; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECPT_F2_4; 1.

SQ SEQUENCE 574 AA; 63620 MW; 801934246B426DF5 CRC64;

Query Match 35.2%; Score 461; DB 4; Length 574;
 Best local similarity 40.1%; Pred. No. 2.3e-36;
 Matches 107; Conservative 33; Mismatches 81; Indels 46; Gaps 12;

QY 1 MARPPSAPPS---LLILLIAQLVGRAAAASAPVCOEITVPMCRGIGYNTLTMNQFNHDTODEAGLE*104
 DB 1 MRDPGAAPLSSIGLCALVIALGALISAGAGQPYHGEKGISVPHGFCQPISTPLCTDI 60
 QY 45 GYVLTMPNQFNHDTODEAGLEVHOFPVLEIQCSPPDLRFELCTMYTPICLPDYHKPLRP 104
 DB 61 ANQNTLLPMLHGTNQEDAGLEVHOFPVLEIQCSPPDLRFELCTMYTPICLPDYHKPLRP 119
 QY 105 CSVCEERAAAGSPILMROYGFAWPERMSCDRLPVLGRDAEVLQMDYNRSEATTAP---PR 161
 DB 120 CRLCERARQGCALMKNKGFQWPERLRNCPVHG--AGEICVQGNISDSGGPGCGFT 177
 QY 162 PEPKPTLPFG-----PGAPASGGECPAGFPVCKREPPVPLKESHPLYNKVRGQV 215
 DB 178 AVPTAYLPLDLPFTALPPG--ASDGRGRPAFPFSCP-RQLKYP-----PYLGYRFLGE- 227
 QY 216 PNCVAVCYOPS-----FSADERTFA 235
 DB 228 RDCGAPC-EPGRANGLMYFKEERRPA 253

RESULT 9

ID Q9U8U6 PRELIMINARY; PRT; 550 AA.
 AC Q9U8U6;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-OCT-2001 (Tremblrel. 18, last annotation update)
 DE Cfz2.
 GN CFZ2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94429803; PubMed=10498678;
 RA Sato A., Kojima T., Ue-Tai K., Miyata Y., Saigo K.;
 RT "Frizzled-3, a new Drosophila mnt receptor, acting as an attenuator
 of Wingleless signaling in wingless hypomorphic mutants."
 RL Development 126:4421-4430 (1999).
 DR EMBL; AB026113; BAA84678.1; -
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000539; Frizzled.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR000832; GPCR secretin.
 DR Pfam; PF01534; Frizzled; 1.
 DR Pfam; PF01392; Fz; 1.
 DR PRINTS; PR00489; FRIZZLED.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS50038; FZ; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECPT_F2_4; 1.
 SQ SEQUENCE 550 AA; 62012 MW; 652968A853B1A69A CRC64;

Query Match 34.4%; Score 451; DB 5; Length 550;
 Best local similarity 38.9%; Pred. No. 2.1e-35;
 Matches 93; Conservative 31; Mismatches 77; Indels 38; Gaps 6;

QY 11 SLLILLIAQLVGRAAAASAPVCOEITVPMCRGIGYNTLTMNQFNHDTODEAGLE*70
 DB 6 SYLFLILGSC--GALFGKQKCEQITLPLCKGIGYNTMSPNSYGHEKQEBAGLEVHOFP 62
 QY 71 WPLVLEIQCSPPDLRFELCTMYTPICLPDYHKPLPPCRSVCEERAAAGSPILMROYGFAWPER 130
 DB 63 YPLVEVGCFQHLKFLCTMYTPICOENYDKPLPCMELCEVARSKCSPIYAKYGFRRPPT 122

QY 131 MGCRLPVLGRDAEVLCDYNRSEATTAPRPPAKP-----TLPG 171
 DB 123 LSCBALPKMS-----DOMSTGNICAAAPDPKPKKHGHHKONONONHNSPDG 174
 QY 172 PP-GAASAGSECPAG-GPFVCKGREPFVPLIKESHPLVYNKRTGOVPCNAVPCYQSFS 228
 DB 175 PEVYSKIDNEVIAGSECCQCTCNQPFQVASE-----SKRVGNVNCAYSCHSPALA 227

RESULT 10

Q90YL7 PRELIMINARY; PRT; 550 AA.
 AC Q90YL7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Frizled-2.
 GN ZF22.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21369720; PubMed=11477686;
 RX Sumnas S., Kim H.J., Hermanson S., Ekker S.C.;
 RT "Zebrafish frizled-2 morphant displays defects in body axis
 elongation.";
 RL Genesis 30:114-118(2001).
 DR EMBL; AF035392; AAK56401.1; -;
 DR InterPro; IPR000539; Frizled.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR000832; GPCR secretin.
 DR Pfam; PF01534; Frizled; I.
 DR PROSITE; PS50038; Fz; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
 SQ SEQUENCE 550 AA; 61748 MW; 7F7A4C92B8E8AAE4 CRC64;

Query Match 32.8%; Score 429.5; DB 13; Length 550;
 Best Local Similarity 45.1%; Pred. No. 2.5e-33;
 Matches 87; Conservative 24; Mismatches 57; Indels 25; Gaps 8;

QY 33 COEITVPMCRGIGYNLTNHPNCFHDTODAGLEVHQMFLVEIQSPDLRFLLCTMYTP 92
 DB 39 CQPTITPLCTDIAYNOTIMPNLVGHYNQEDAGLEVHQMFLVEIQSPDLRFLLCTMYTP 98
 QY 93 ICLPDYHKLPCRSVCERAKAGCSPLMRQYGFAMPERMSCDRLPYLGRDAEVLCDYNR 152
 DB 99 VCTV-LEKA1PCRSICERAKAGCEVLMNKFQWPEALRCEHPVLG-DGHI-CVGQND 155
 QY 153 SEATTAPR-PPPAKT--LPFGAPASGSECPAGPFVCKREPFVPLIKESHPLYNK 209
 DB 156 SWATVSPVMPFPGTSPVLYSTPDKPF--RCPS-----TLKV--PAYIS 196
 QY 210 VRTGVPCNAVPC 222
 DB 197 YKFLGEPDGCAPC 209

RESULT 11

Q9NL45 PRELIMINARY; PRT; 872 AA.
 AC Q9NL45;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Frizled homolog.
 GN CIFR2.
 OS Clona intestinalis.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 OC Phlebobranchia; Clonidae; Clona.

OK NCBI_TaxID=7719;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Imai K., Takada N., Satch N., Satch Y.;
 RT "An essential role of beta-catenin in the endoderm specification of
 ascidian embryo.";
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB031542; BAA92184.1; -;
 DR InterPro; IPR000539; Frizled.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR000832; GPCR secretin.
 DR Pfam; PF01534; Frizled; I.
 DR Pfam; PF01392; Fz; 1.
 DR PRINTS; PR00489; FRIZLED.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PS50038; Fz; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
 SQ SEQUENCE 872 AA; 96568 MW; 980E086E6E0D269C CRC64;

Query Match 32.5%; Score 426; DB 5; Length 872;
 Best Local Similarity 40.3%; Pred. No. 8.8e-33;
 Matches 98; Conservative 30; Mismatches 77; Indels 38; Gaps 12;

QY 9 PPSLLILLALQVGRRAAASKAPVCOEITVPMCRGIGYNLTN--PNCFHDTODAGLE 66
 DB 112 PP-----ISGLSGRGCTG---VCEPIQVPMCIDIGVFTMSVPSYIYD-QKEAAS 160
 QY 67 VHQFMFLVEIQSPDLRFLLCTMYTPICLDYHKLPCRSVCERAKAGCSPLMRQYGA 126
 DB 161 VIQFGPLTKCAEEMKLVCSVTPICTPGYGFPLPFCRPFCEAKAGCEPILKKYDRT 220
 QY 127 WPERNSCDRLP-VLGRDAEVLCDYNRSEATTAP--PPPPAK---PTLPGPGA----- 175
 DB 221 WNLFLPCQKFPDSQGNKP--CLHFNRS-ATEEPAVPRTITKGSKTPPGSPVASVTH 277
 QY 176 ---PASGCECPAGPFVCKREPFVPLIKESHPLYNKRTGOVPCNAVPCYQSFSADR 232
 DB 278 PYKPLNG--CP-----CACARWVKITWKDPLVGYKVTGGVPCNAVPCAMPCKSPYFSEER 329

RESULT 12

Q90ZT3 PRELIMINARY; PRT; 559 AA.
 AC Q90ZT3;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Frizled 7b.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Emeljanov A., Sleptsova-Friedrich I., Fong I., Korzh V.;
 RT "Frizled 7b interacts with Wnt5 in the enveloping layer of embryonic
 zebrafish.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF36123; AAK49948.1; -;
 DR InterPro; IPR002086; Aldhyde_dehydr.
 DR InterPro; IPR000539; Frizled.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR000832; GPCR secretin.
 DR Pfam; PF01534; Frizled; I.
 DR Pfam; PF01392; Fz; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
 DR PROSITE; PS50038; Fz; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.

SEQUENCE 559 AA; 63695 MW; 85667E255AA50DB2 CRC64;

Query Match 31.3%; Score 410.5; DB 13; Length 559;

Best Local Similarity 41.8%; Pred. No. 1.7e-31; Indels 23; Gaps 4;

Matches 81; Conservative 25; Mismatches 65; Indels 23; Gaps 4;

QY 33 COEITVPMCRGIGYNTLHMPNQHDTQDEAGLEVHOFMPLVEIQSPDLRFELCTMYTP 92
DB 45 CQDISIPLCIDIAVNOQIMENLGHNTQEDAGLEVHOFYPLVKVQCSMDLKFELCSMYAP 104
QY 93 ICLPDYHKLPPCRSVCEKAKGCSPLMRQYGFAMPFERMSCDRLPVLGRDAEVLCDMYNR 152
DB 105 VCTV-LEQAIIPCRSLCERARQCEALMKNKFGQWPERLRCENFPVHG--AGEICVGQNT 161
QY 153 SEATTAPRRFPKPTL-----PGPPGAPASGGECPAGFPVCKCRBPFPVLKESHPLYN 208
DB 162 SDAGSPTSNPTFYPELLITLQPNLVARNQOFTCP-----LQLKVPYTL 205
QY 209 KVRTGOVNCAPVC 222
DB 206 KYHFMGEKDCGAPC 219

RESULT 13

ID Q98S12 PRELIMINARY; PRT; 559 AA.
AC Q98S12;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Frizzled 7 protein (Fragment).
GN FZ7.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_Taxid=7955;
RX SEQUENCE FROM N.A.
RX MEDLINE=21184123; PubMed=11287199;
RA El-Messaoudi S., Renucci A.;
RT Expression pattern of the frizzled 7 gene during zebrafish embryonic
RT development.";
RL Mech. Dev. 102:231-234 (2001).
DR EMBL: AJ301617; CAC3733.1; -
DR InterPro: IPR002086; Aldehyde_dehydr.
DR InterPro: IPR000539; Frizzled.
DR InterPro: IPR000832; GPCR_secretin.
DR Pfam: PF01534; Frizzled; 1.
DR Pfam: PF01392; Fz; 1.
DR PRINTS: PR00489; FRIZZLED.
DR SMART: SM00063; FRI; 1.
DR PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE: PS50038; FZ; 1.
DR PROSITE: PS50261; G_PROTEIN_RECEPTOR_F2_4; 1.
FT NON TER 1
FT SEQUENCE 559 AA; 63719 MW; 25F243A465F04D4B CRC64;

Query Match 31.2%; Score 408.5; DB 13; Length 559;

Best Local Similarity 41.8%; Pred. No. 1.7e-31;

Matches 81; Conservative 25; Mismatches 65; Indels 23; Gaps 4;

QY 33 COEITVPMCRGIGYNTLHMPNQHDTQDEAGLEVHOFMPLVEIQSPDLRFELCTMYTP 92
DB 45 CQDISIPLCIDIAVNOQIMENLGHNTQEDAGLEVHOFYPLVKVQCSMDLKFELCSMYAP 104
QY 93 ICLPDYHKLPPCRSVCEKAKGCSPLMRQYGFAMPFERMSCDRLPVLGRDAEVLCDMYNR 152
DB 105 VCTV-LEQAIIPCRSLCERARQCEALMKNKFGQWPERLRCENFPVHG--AGEICVGQNT 161
QY 153 SEATTAPRRFPKPTL-----PGPPGAPASGGECPAGFPVCKCRBPFPVLKESHPLYN 208

DB 162 SDAGSPTSNPTFYPELLITLQPNLVARNQOFTCP-----LQLKVPYTL 205
QY 209 KVRTGOVNCAPVC 222
DB 206 KYHFMGEKDCGAPC 219

RESULT 14

ID Q80FM3 PRELIMINARY; PRT; 557 AA.
AC Q80FM3;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Frizzled-7A.
GN FZ7A.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_Taxid=7955;
RX SEQUENCE FROM N.A.
RX Sumana S., Kim H.J., Hermanson S.B., Ekker S.C.;
RT "Zebrafish frizzled-7A is expressed maternally and zygotically during
RT embryogenesis.";
RT Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Emejanov A., Sleptsova-Friedrich I., Fong I., Korzh V.;
RT "Frizzled 7b interacts with Wnt5 in the enveloping layer of embryonic
RT zebrafish.";
RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF437316; AAL87635.1; -
DR EMBL: AF336124; AAM00192.1; -
DR SEQUENCE 557 AA; 63475 MW; DEF32BF11596C83 CRC64;

Query Match 30.8%; Score 403; DB 13; Length 557;

Best Local Similarity 41.0%; Pred. No. 9.2e-31;

Matches 80; Conservative 28; Mismatches 61; Indels 26; Gaps 6;

QY 33 COEITVPMCRGIGYNTLHMPNQHDTQDEAGLEVHOFMPLVEIQSPDLRFELCTMYTP 92
DB 45 CQDISIPLCIDIAVNOQIMENLGHNTQEDAGLEVHOFYPLVKVQCSMDLKFELCSMYAP 104
QY 93 ICLPDYHKLPPCRSVCEKAKGCSPLMRQYGFAMPFERMSCDRLPVLGRDAEVLCDMYNR 152
DB 105 VCTV-LEQAIIPCRSLCERARQCEALMKNKFGQWPERLRCENFPVHG--AGEICVGQNT 161
QY 153 S-EATTAPRRFP---PAKPTLPGPPGAPASGGECPAGFPVCKCRBPFPVLKESHPLY 207
DB 162 SDPDVTTNPTFYIPRPFPRHITRQNA-----FTCP-----LQLTVPSY 203
QY 208 NKVRTGOVNCAPVC 222
DB 204 LNVHFLGANKGAPC 218

RESULT 15

ID Q8TAN2 PRELIMINARY; PRT; 591 AA.
AC Q8TAN2;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Frizzled homolog 9 (Drosophila).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Carnivora; Homiidae; Homo.
OC NCBI_Taxid=9606;
RX SEQUENCE FROM N.A.
RX TISSUE=BRAIN;

RA Strausberg R.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC026333; AAH26333.1;
 SQ SEQUENCE 591 AA; 64519 MW; 9E341E2E33F70C4C CRC64;

Query Match 30.6%; Score 401.5; DB 4; Length 591;

Best Local Similarity 37.4%; Pred. No. 1,4e-30; Indels 33; Gaps 7;

Matches 89; Conservative 28; Mismatches 88; Indels 33; Gaps 7;

QY 15 LLLAQLVGRRAAASK-----APVCOEITVPMCRGIGYNLTMPNQFNHDTQDEA 63
 DB 10 LLLMQLLAGGALLLEIGRDPERGRGALPCQAVEIIMCRGIGYNLTMRNLGHTSGEA 69
 QY 64 GLEVHOFWPLVEIQSPDLRFELCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPLMRQY 123
 DB 70 AAELEAFAPLVQYCHSHLRFELCSLYAPMCTDQVSTPIPACRPMCEQARLRCAPIMEQF 129
 QY 124 GFAMPERMGCDDLPLVIGRDAEVLQMDYNRSEATTAPRP-----FPAKPTLPGPGCAPA 177
 DB 130 NFGWPDLSLDCARLPT-RNDPHALCMEAPEN-ATAGPAEPHKGIGMLPVAPRPAPRPDGLG 187
 QY 178 SGGECPAGGPFVQCKREPFVPIKESHPLYNKVRTGQVPCAVPCYQPSFSADERTFA 235
 DB 188 PG---AGSGGTCTENREKF-----QYVEXSRSCAPRCG-PGVVFWWSRDKDFA 231

Search completed: May 19, 2003, 16:35:38
 Job time : 37 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 22, 2003, 21:24:29 ; Search time 2664 Seconds
(without alignments)
2567.252 Million cell updates/sec

Title: US-09-847-102A-68
Perfect score: 1310
Sequence: 1 MARPDSPAPSLILLIAQL.....FNCAVPCYQSPFSADERTFA 235

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database :
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1310	100.0	2334	9 HSU43318	U43318 Human putat
2	1306	99.7	3134	9 AB043702	AB043702 Homo sapi
3	1306	99.7	177733	9 AC096772	AC096772 Homo sapi
4	1250	95.4	179788	2 AC101915	AC101915 Mus muscu
5	1143	87.3	1734	10 AF272146	AF272146 Mus muscu
6	1131.5	86.4	746	9 HSJ329758	HSJ329758 Homo sapi
7	1017	77.6	821	9 HSJ33422	AJ333422 Homo sapi
8	832.5	63.5	2380	5 AF300716	AF300716 Xenopus l
9	824	62.9	2085	6 AX367099	AX367099 Sequence
10	824	62.9	3195	9 AB043703	AB043703 Homo sapi
11	824	62.9	166007	9 HSB4425A6	AL121749 Human DNA
12	823.5	62.9	2421	10 MMU43321	U43321 Mus musculu
13	823.5	62.9	215585	2 AF108777	AF108777 Mus muscu
14	802	61.2	1851	5 AF017177	AF017177 Xenopus l
15	801	61.1	1740	5 AF117389	AF117389 Dario rer
16	801	61.1	2249	5 AF060697	AF060697 Dario rer
17	800	61.1	2554	5 AF039412	AF039412 Dario rer
18	796	60.8	1779	5 AF117387	AF117387 Dario rer
19	796	60.8	3230	5 AF033110	AF033110 Xenopus l
20	794	60.6	1731	5 AF117390	AF117390 Dario rer
21	794	60.6	2522	5 AF060696	AF060696 Dario rer
22	794	60.6	2523	5 AF039410	AF039410 Dario rer
23	621	47.4	2085	3 DMU65589	U65589 Drosophila
24	621	47.4	175963	3 AC009379	AC009379 Drosophila
25	621	47.4	180387	3 AC009378	AC009378 Drosophila
26	621	47.4	279530	3 AE003518	AE003518 Drosophila
27	543.5	41.5	62712	2 AC018167	AC018167 Drosophila
28	542.5	41.4	21732	2 AC019377	AC019377 Drosophila
29	479.5	36.6	2112	10 AF206321	AF206321 Mus muscu
30	479.5	36.6	169930	10 AL672269	AL672269 Mouse DNA
31	477	36.4	1888	9 AB017364	AB017364 Homo sapi
32	477	36.4	1923	9 HUMPRIZ	L37882 Human frilz
33	477	36.4	161566	2 AC103703	AC103703 Homo sapi
34	476	36.3	182182	2 AC091152	AC091152 Homo sapi
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36	461	35.2	3067	9 BC015915	BC015915 Homo sapi
37	461	35.2	3851	9 AB017365	AB017365 Homo sapi
38	461	35.2	71173	9 AC069148	AC069148 Homo sapi
39	457	34.9	1750	9 AB010881	AB010881 Homo sapi
40	451	34.4	1653	3 AB026113	AB026113 Caenorhab
41	447	34.1	113915	2 AC120200	AC120200 Dario rer
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RESULT 1

ALIGNMENTS

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 DEFINITION Human putative transmembrane receptor (frizzled 5) mRNA, complete cds.
 ACCESSION U43318
 VERSION U43318.1 GI:1151251
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 2334)
 AUTHORS Wang, Y., Macke, J.P., Abella, B.S., Andreasen, K., Worley, P., Gilbert, D.J., Copeland, N.G., Jenkins, N.A. and Nathans, J.
 TITLE A large family of putative transmembrane receptors homologous to the product of the Drosophila tissue polarity gene frizzled
 JOURNAL J. Biol. Chem. 271 (8), 4668-4476 (1996)
 MEDLINE 96224032
 PUBMED 8626800
 REFERENCE 2 (bases 1 to 2334)
 AUTHORS Abella, B., Wang, Y., Macke, J.P. and Nathans, J.
 JOURNAL Submitted (14-DEC-1995) Jeremy Nathans, Molecular Biology and Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street, Baltimore, MD 21205
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 Score: 1310.00 Matches: 235
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 Best Local Similarity: 100.00% Mismatches: 0
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 Gaps: 0
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 QY 21 ValGlyATGAlaAlaAlaSerLysAlaProValCySGInGluIleThrValProMet 40
 DB 381 GTGGGCGGGGCGGCGCGGTCCAGGCGCCGCGGTGTGTCAGGAATATCATCGGTGCCCATG 440

QY 41 CysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
 DB 441 TGCCGCGGCATCGGCTACCACTGACGACATGCGCAACCGTTCAACACGACGCGAG 500
 QY 61 AepGluAgiValGluGluValHisGlnPheThrProLeuValGluIleGlnCysSerPro 80
 DB 501 GACGAGGCGGCGCTGGAGGTGACCAAGTCTGGCGCGGTGGAGATCAATGCTGCGCG 560
 QY 81 AspLeuArgPhePheLeuCyEThMetTyrThrProIleCysLeuProAspTyrHisLys 100
 DB 561 GACCTGCGCTTCTTCTATGACATGATGACAGCGCCCATCTGTGCGCGACTACACAG 620
 QY 101 ProLeuProProCysArgSerValCysGluArgAlaLysAlaGlyCysSerProLeuMet 120
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 QY 121 ArgGlnTyrGlyPheAlaThrProGluArgMetSerCysAspArgLeuProValLeuGly 140
 DB 681 CGCAGATGCGGCTTGTGCTGCGCGCGAGCGATGAGCTGCGACCGCTTCCGAGTGGGC 740
 QY 141 ArgAspAlaGluValLeuCyMetAspTyrAsnArgSerGluAlaThrThrAlaProPro 160
 DB 741 CGCAGCGCGGAGGTCTCTGTGATGATTACACCGACGACGACGACGACGCGCGCC 800
 QY 161 ArgProPheProAlaLysProThrLeuProGlyProProGlyAlaProAlaSerGly 180
 DB 801 AGGCTTTCACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 860
 QY 181 GluCySProAlaGlyValProPheValCysLysCysArgGlyPheProPheValProIleLeu 200
 DB 861 GAATGCCCCGCTGGGCGCGCTGCTGTGACAGGTGTGCGAGCGCTTGTGCTGCTGCTG 920
 QY 201 LysGluSerHisProLeuTyrAsnLysValArgThrGlyGlnValProAsnCysAlaVal 220
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 QY 221 ProCysTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
 DB 981 CCTGCTACGACGCGCTTCTGATGCGGACGACGACGACGACGACGACGACGACGACG 1025
 RESULT 2
 AB043702 3134 bp mRNA linear PRI 20-JUN-2001
 LOCUS Homo sapiens FZ05 mRNA for seven-transmembrane receptor Frizzled-5, complete cds.
 DEFINITION
 ACCESSION AB043702
 KEYWORDS AB043702.1 GI:14495150
 SOURCE Homo sapiens cDNA to mRNA, clone_id: human fetal lung cDNA library (CLONTECH).
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 3134)
 AUTHORS Saitoh, T., Hirai, M. and Katoh, M.
 TITLE Molecular cloning and characterization of human Frizzled-5 gene on chromosome 2q33.3-q34 region
 JOURNAL Int. J. Oncol. 19 (1), 105-110 (2001)
 MEDLINE 21301556
 REFERENCE 2 (bases 1 to 3134)
 AUTHORS Katoh, M.
 TITLE Direct Submission
 JOURNAL Submitted (24-MAY-2000) Masaru Katoh, National Cancer Center, Genetics Division, Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045, Japan (E-mail: mkatoh@nci.go.jp, Tel:81-3-3542-2511 (ex.4402), Fax:81-3-3541-2685)
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QY      81 AspleuAtrPhePheLeuLeuCyseThrMetTYrThrProIleCysLeuProAspTYrHisLys 100
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      806 CGCGAGCGCGAGAGTCTCTGATGATTAACAAGCGAGAGCGACCAACGCGCGCGCG 865
QY      161 ArgProPheProAlaLysProThrIleuProGlyProProGlyAlaProAlaSerIleGly 180
      866 AGGCGCTTCCAGCCACACCCCTTCACAGCGCGCGCGCGCGCGCGCGCGCGCGCG 925
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RESULT 3
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LOCUS      177733 bp      DNA      linear      PRI 23-MAR-2002
DEFINITION Homo sapiens BAC clone RP11-801F7 from 2, complete sequence.
ACCESSION      AC096772.3
VERSION      AC096772.3 GI:19424671
KEYWORDS      HTG.
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 177733)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
9847074
2 (bases 1 to 177733)
Belter,E., Cotton,M. and Spalding,L.
The sequence of Homo sapiens BAC clone RP11-801F7
Unpublished (2001)
3 (bases 1 to 177733)
Waterston,R.H.
Direct Submission
Submitted (25-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 177733)
Waterston,R.H.
Direct Submission
Submitted (14-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 177733)
Waterston,R.H.
Direct Submission
Submitted (15-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 177733)
Waterston,R.
Direct Submission
Submitted (23-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 14, 2002 this sequence version replaced gi:16604097.

----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0801F07
Drafting Center: WIBR
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPC1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E., Tateo, M., Cattanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-196E10, 2000 bp overlap; the clone sequenced to the right is RP11-372C13, 2000 bp overlap. Actual end of this clone is at base position 22072 of RP11-372C13.

Polymorphisms have been identified between AC009409, AC079767, AC083900 and AC096772.

Data from AC009409 and AC022576 was used to finish this clone, AC096772.

FEATURES
The sequence of AC036191 has been incorporated into AC096772.
Location/Qualifiers

source

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Alignment Scores:

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US-09-847-102a-68 (1-235) x AC096772 (1-177733)

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 Direct Submission
 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 179789)
 Biren, B., Nishubum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barua, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Deakell, K., Dewar, K., Diaz, J.S., Dodge, S., Fato, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gadyana, S., Goid, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kats, A., Kataras, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunhkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tsafaye, S., Theodore, J., Tophan, K., Travers, M., Vassiliou, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Aug 21, 2002 this sequence version replaced gi:17060691.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L17740
 Center clone name: 388 p.13
 ----- Summary Statistics
 Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye, 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 170170 bases at least Q40
 Consensus quality: 174390 bases at least Q30
 Consensus quality: 176052 bases at least Q20
 Insert size: 170000; agarose-efp
 Insert size: 177888; sum-of-ctnigs
 Quality coverage: 4.9 in Q20 bases; agarose-efp
 Quality coverage: 4.7 in Q20 bases; sum-of-ctnigs

 * NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
 945: contig of 945 bp in length

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 DEFINITION Xenopus laevis frizzled-5 mRNA, complete cds.
 ACCESSION AF300716
 VERSION AF300716.1 GI:14009632
 KEYWORDS
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 ORGANISM
 Xenopus laevis.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 2380)
 Sumanae, S. and Ekker, S.C.
 TITLE
 Xenopus frizzled-5: a frizzled family member expressed exclusively
 in the neural retina of the developing eye
 JOURNAL
 Mech. Dev. 103 (1-2), 133-136 (2001)
 PUBMED
 21233029
 REFERENCE
 2 (bases 1 to 2380)
 Sumanae, S. and Ekker, S.C.
 TITLE
 Direct Submision
 JOURNAL
 Submitted (28-AUG-2000) Department of Genetics, Cell Biology and
 Development, University of Minnesota, 6-160 Jackson Hall, 321
 Church St. SE, Minneapolis, MN 55455, USA
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 Best Local Similarity: 64.46% Mismatches: 37
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 US-09-847-102a-68 (1-235) x AF300716 (1-2380)
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 QY 33 CysGlnGluIleThValProMetCysArgGlyIleGlyTyrAsnLeuThriSmetPro 52
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 QY 173 ProGlyAlaProAlaSerGlyGlyGluCysProAlaGlyGlyProPheValCysLeuCys 192
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 QY 213 GlyGlnValProAsnCysAlaValProCysGlyTyrGlnProSerPheSerAlaAspGluArg 232
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 AX367099 2085 bp DNA linear PAT 16-FEB-2002
 LOCUS AX367099
 DEFINITION Sequence 18 from Patent WO0198354.
 ACCESSION AX367099
 VERSION AX367099.1 GI:18855301
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
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 Griffin, J.A., Kallick, D.A., Tribouley, C.M., Yue, H., Nguyen, D.B.,
 Tang, Y.T., Lai, P., Policky, J.L., Azimzai, Y., Lu, D.A., Graul, R.,
 Yao, M.G., Burford, N., Hafalia, A.J., Baughn, M.R., Bandman, O.,
 Patterson, C., Yang, J., Xu, Y., Warren, B.A., Ding, L. and
 Sanjana, M.S.
 TITLE
 Receptors
 JOURNAL
 Patent: WO 0198354-A 18 27-DEC-2001;
 Incyte Genomics, Inc. (US)
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 location/Qualifiers
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 /note="Incyte ID No: 1534444CB1"
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 Alignment Scores:
 Pred. No.: 1.91e-40 Length: 2085
 Score: 824.00 Matches: 161
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 Best Local Similarity: 59.85% Mismatches: 39
 Query Match: 62.90% Indels: 48
 DB: 6 Gaps: 8
 US-09-847-102a-68 (1-235) x AX367099 (1-2085)


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Db      453 GACTCAACACCGACGACCTAACACACCGCGCGCCAGCGCGCGCGCGCGCGCTGCGCGCG 512
Qy      166 LysProThrLeuProGly-----ProProGly 174
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Qy      206 LeuTyrAsnLysValArgThrGlyGluValProAsnCyAlaValProCySerTyrGlnPro 225
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Qy      226 SerPheSerAlaAspGluArgThrPhe 234
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RESULT 11
LOCUS   HSB425A6/c 166007 bp DNA linear PRI 21-JUN-2002
DEFINITION Human DNA sequence from clone RP11-425A6 on chromosome 10, complete
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ACCESSION AL121749
VERSION   AL121749.14 GI:21541283
KEYWORDS  HTG.
SOURCE    human.
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          Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Eumetazoa; Eutheria; Primates; Catarrhini; Homiidae; Homo.
          1 (bases 1 to 166007)
          Heath, P.
REFERENCE Direct Submission
          Submitted (21-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
          Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
          humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
          On Jun 23, 2002 this sequence version replaced gi:17530251.
          During sequence assembly data is compared from overlapping clones.
          Where differences are found these are annotated as variations
          together with a note of the overlapping clone name. Note that the
          variation annotation may not be found in the sequence submission
          corresponding to the overlapping clone, as we submit sequences with
          only a small overlap as described above.
          The following abbreviations are used to associate primary accession
          numbers given in the feature table with their source databases:
          Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
          on the WORMPEP database can be found at
          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
          was generated from part of bacterial clone contigs of human
          chromosome 10, constructed by the Sanger Centre Chromosome 10
          Mapping Group. Further information can be found at
          http://www.sanger.ac.uk/HGP/Chr10
          ----- Genome Center
          Center: Wellcome Trust Sanger Institute
          Center code: SC
          Web site: http://www.sanger.ac.uk
          Contact: humquery@sanger.ac.uk

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This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. RP11-425A6 is from
the library RPCI-11.2 constructed by the group of Pieter de Jong.
For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: BAC3.6.
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Query Match: 62.90% Indels: 48
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US-09-847-102a-68 (1-235) x HSB425A6 (1-166007)
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Qy      49 ThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHis 68
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Qy      89 MetTyrThrProIleCyLeuProAspTyrHisLysProLeuProProCyAspSerVal 108
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Qy      166 LysProThrLeuProGly-----ProProGly 174
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Df	130921	TGCGAGCCCCGGGTGCAGTGCCGCGGCGCTATGTGTAGCGTGTCCAGCGAGCCCAACCCG	130867						
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Df	130861	CCTTCACMACCGGGTCTCAAAGACAGCCAGACTCACTACGTGCGCGCTGCTGCCACAACC	130802						
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DEFINITION	Mus musculus putative transmembrane receptor (frizzled 8) gene,								
ACCESSION	U43321								
VERSION	U43321.1								
KEYWORDS	GI:1151259								
SOURCE	Mus musculus.								
ORGANISM	Mus musculus.								
REFERENCE AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.								
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JOURNAL MEDLINE PUBLISHED	Wang,Y., Macke,J.P., Abella,B.S., Andreasson,K., Worley,P., Gilbert,D.J., Copeland,N.G., Jenkins,N.A. and Nathans,J. A large family of putative transmembrane receptors homologous to the product of the Drosophila tissue polarity gene frizzled J. Biol. Chem. 271 (8), 4468-4476 (1996) 96224032 8626800								
AUTHORS	2 (bases 1 to 2421)								
JOURNAL TITLE	Abella,B., Wang,Y., Macke,J.P. and Nathans,J. Direct Submission Submitted (14-DEC-1995) Jeremy Nathans, Molecular Biology and Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street, Baltimore, MD 21205								
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BASE COUNT	403 a	772 c	779 g	467 t					
ORIGIN									
Alignment Scores:									

Pred. No.: 2,376-40	Length: 2421
Score: 823.50	Matches: 159
Percent Similarity: 69.06%	Conservative: 24
Best Local Similarity: 60.00%	Mismatch: 39
Query Match: 62.86%	Indels: 43
DB: 10	Gaps: 8

US-09-847-102A-68 (1-235) x MMU43321 (1-2421)

OY	11	SerLeuLeu-----LeuLeuLeuLeuAlaGlnLeuValGIYAArgAlaAlaAspSer	28
Db	218	TGGCTCCTAGACCGCCTTGCGGTGCTACAGCGCTCTAGCCGCCTGCGCGCTTCGGCC	277
OY	29	LysAlaProValCYSGInGUllleThyValPrometCYsaArgGlyIleGlyTYrTrsnLeu	48
Db	278	AAGAGCTGGCGGTGCAGAGATCATCGGTGCCGTGTGTCAAAAGCATGGTTACAACATAC	337
OY	49	ThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGlnValHis	68
Db	338	ACTTACATGCCCAACCACTTACCACCAACACACACGCAAGTAGAGCGCGCTTAGAGGTGCAC	397
OY	69	GlnPheTrpProLeuValGluIlleGlnCYsseerProAspLeuArgPhePheLeuCysThr	88
Db	398	CAGTTTTGGCGGTGTGGATACAGTACGTCCCCGGACCTCAAGTCTTTCTGTGTAGC	457
OY	89	MetTYrThrProIleCYseLeuProAspTYrHisLysProLeuProProCYsaArgSerVal	108
Db	458	ATGTACACGCCCATCTGCTGTGAGAGACTACAGAAGCCTTCGCCCTTGTGCTGTG	517
OY	109	CysGluARgAlaLYsAlaGlyCYsaSerProLeuMetArGlnTYrGlyPheAlaTrpPro	128
Db	518	TGTGAACCGCGCAAGCGCGGTGCGCGCTCATGCCAGTACAGGCTTTGCTTGCGCT	577
OY	129	GluARgMetSerCYsaSPArgLeuProValLeuGlyArGAspAlaGluValLeuCysMet	148
Db	578	GACCGCATGCGCTGTGATCGTGTGCGSAGAGAGGCG---AACCGGACACTGTGTGATG	634
OY	149	AspTYraNaARgSerGluAlaThrThirAla-----ProProArgProPheProAla	165
Db	635	GACTACAAACCGCACCGACCTCACACACGCGCGCCACGACCGCGCGCTGCTCG	694
OY	166	LysProThrLeuProGly-----ProProGly	174
Db	695	CCGCTCTCT--CCCGGCGAGACGCCGCCCTCTGTGACGCGCCACAGCCGCCGCCAGGG	751
OY	175	Ala-----	175
Db	752	GCCAGAGCCCCACATCTGTCGGCGGACAGTAGAGGGGACACGGGGACGGCGCTCGGCC	811
OY	176	ProAlaSerGlyGlyGluCYs----ProAlaGlyTyProPheVal-----	189
Db	812	CCTTCGCGCGCGGGAGAGGACGAGCGCCCTGTGTGGCGGCGGTGCTCTCCCTGCGAGCGGGAG	871
OY	190	CysLysCYsaArgGluProPheValProIleLeuLysGlnUserHisProLeuTYrAsnLys	209
Db	872	TGCGAGTCCCGCGCGCCCATGATGAGCGCTGTCCACGAAACCCACCGCTCTACAAACGC	931
OY	210	ValArGThrGlyGlnValProAsnCysAlaValProCYrTYrGlnProSerPheSerAla	229
Db	932	GTCAAAGCCGGGCGAGATGCCCACTGTGCGCTGCGCTGCCACACACCCTTTTATAGCAG	991
OY	230	AspGluARgThrPhe	234
Db	992	GATGAGCGCGCCTTC	1006

RESULT 13

AC108777

LOCUS

DEFINITION Mus musculus clone RP23-368H22, WORKING DRAFT SEQUENCE, 17 ordered pieces.

ACCESSION AC108777

VERSION AC108777.2

KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT; HTGS FULLTOP.

21585 bp DNA linear

HTG 05-JUN-2002


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Db      505 ATTATCCGCACAAAAAGCGGCGCGCCAGCGCTCGACCAATAAAGAAATTAAGCCC 564
Qy      182 CysProAlaGlyGlyProPheValCysLysCysArgGluProPheValProIleLeuLys 201
      565 TCCGAGCCCGGGC-----TCCCACTGTCCGCGCGCGATGCTGCCGCTGAACAGC 612
Qy      202 GluSerHisProLeuTyrAsnLysValArgThrGlyGlnValProAsnCysAlaValPro 221
      613 GATCGACACCCGCTCTACCAACCGCGTTAAGACGCGTCAAAATCCCAACTGCCGCATGCCA 672
Qy      222 CysTyrGlnProSerPheSerAlaAspGluArgThrPhe 234
      673 TGTCAACACCCATATTATTAGCGAGATGAGCGGACTTTT 711
Db
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Search completed: May 23, 2003, 05:26:08
Job time : 2758 secs


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FT      /+tag= a
XX      WO9739357-A1.
XX      23-OCT-1997.
XX      11-APR-1997; 97WO-US06049.
XX      12-APR-1996; 96US-0015307.
XX      (UJJO ) UNIV JOHNS HOPKINS.
XX      (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
XX      Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J,
XX      Nusse R, Samos CH, Wangy;
XX
XX      WPI; 1997-526631/48.
XX      P-PSDB; AAW31271.
XX
XX      Identification of Wnt receptor binding modulators - useful for
XX      treatment of cancer and growth, development or proliferation related
XX      disorders
XX
XX      Disclosure; Page 36-37; 61pp; English.
XX
XX      This sequence comprises novel human frizzled gene 5 (Hfz5)
XX      CC that encodes a transmembrane receptor, frizzled-5 (see AAW31771), a
XX      CC Wnt receptor (WntR). Novel frizzled family members have been
XX      CC identified in Drosophila, mouse, human and Caenorhabditis (see
XX      CC AAT89885-92) and are considered to be Wnt receptors. Wnt receptors
XX      CC can be used in a novel, claimed method of screening for compounds
XX      CC which modulate the binding of a Wnt polypeptide (secreted proteins
XX      CC involved in cell-to-cell signaling) to a Wnt receptor. Wnt is
XX      CC involved in (mammary) cancer and other processes involving growth,
XX      CC development and proliferation (both normal and abnormal).
XX      CC Modulators identified by the claimed method are useful for
XX      CC treatment of diseases related to these conditions.
XX
XX      Sequence 2334 BP; 356 A; 803 C; 736 G; 439 T; 0 other;
XX
XX      Alignment Scores:
XX      Pred. No.: 6,2e-84 Length: 2334
XX      Score: 1310.00 Matches: 235
XX      Percent Similarity: 100.00% Conservative: 0
XX      Best Local Similarity: 100.00% Mismatches: 0
XX      Query Match: 100.00% Indels: 0
XX      DB: 18 Gaps: 0
XX
XX      US-09-847-102A-68 (1-235) x AAT89889 (1-2334)
XX
XX      1 MetAlaArgProAspProSerAlaProProSerLeuLeuLeuLeuLeuAlaGlnLeu 20
XX      321 ATGGCTCGGCGCTGACCAATCCGCGCGCCCTCGCTGCTGCTGCTGCGGCGACG 380
XX
XX      21 ValGlyArgAlaAlaAlaAlaSerLysAlaProValCysGlnGlnLeuThrValProMet 40
XX      381 GTGGCGCGGCGCGCGCGCGCTGCAAGCGCCCGGTGTGCAGAAATCAAGTGCCCATG 440
XX
XX      41 CysArgGlyTyrIleGlyTyrTrpLeuLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
XX      441 TGCCTCGGCGATCGCTGACCACTGACGACGACATGCGCAACAGTTCAACACGACGACG 500
XX
XX      61 AspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGlnIleGlnCysSerPro 80
XX      501 GACGAGCGGCGCGCTGAGGTGACCACTGCTGCGCCCTGCTGAGATCCATGCTGCGCG 560
XX
XX      81 AspLeuArgPhePheLeuCysThrMetTyrThrProIleCysLeuProAspTyrHisLys 100
XX      561 GACCTCGCTTCTTCTATGCACTATGATACACCCCATCTGCTGCGCCACATCCACAAG 620
XX
XX      101 ProLeuProProCysArgSerValCysGluArgAlaAlaGlyCysSerProLeuMet 120
XX      621 CCGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 680

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XX      121 ArgGlnTyrGlyPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuGly 140
XX      681 CGCGAGTACGGCTTGGCTTGGCGCGCGCGCGCAATGACTGCAACCGCTCCCGGTGCTGGGG 740
XX
XX      141 ArgAspAlaGluValLeuCysMetAspTyrTrpAsnArgSerGlnAlaThrThrAlaProPro 160
XX      741 CGCGAGCGCGGAGGTCTCTGATGATTAACAACCGACGAGGCCACACGCGCGCGCGCG 800
XX
XX      161 ArgProPheProAlaLysProThrLeuProGlyProProGlyAlaProAlaSerGlyGly 180
XX      801 AGGCTTTTCCAGCCAGCCACCTTCCAGGCCCGCGAGGGGCGCGCGCTCGGGGGGG 860
XX
XX      181 GluCysProAlaGlyGlyProPheValCysLysCysArgGluProPheValProIleLeu 200
XX      861 GAATGCGCGCGCTGGGGGGCGCGTGTGTCGCAAGTGTGCGAGCCCTTGCGTCCATTCTG 920
XX
XX      201 LysGluSerHisProLeuTyrAsnLysValArgThrGlyGlnValProAsnValAlaVal 220
XX      921 AAGGAGTACACCCGCTCTACAAACAGGTGCGAGCGGCGCAGTGTCCCAACTGCGCGTGA 980
XX
XX      221 ProCysTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
XX      981 CCTGCTACACCGCTCTTCACTGCTCCAGACGCGCAGCTTCC 1025
XX
XX      RESULT 2
XX      ID ABK15174 standard; DNA; 2085 BP.
XX      AC ABK15174;
XX      DT 23-APR-2002 (first entry)
XX      DE Human REPTR 6 cDNA sequence.
XX
XX      REPTR; human; antiinflammatory; cytostatic; immunosuppressive;
XX      KW antiviral; anti-HIV; antiarthritic; anticonvulsant; nootropic;
XX      KW neuroprotective; antiallergic; antibody; immunogen; endometriosis;
XX      KW gastrointestinal disorder; gastritis; oesophageal carcinoma;
XX      KW Crohn's disease; irritable bowel syndrome; ulcerative colitis;
XX      KW endocrine disorder; hypothalamus disorder; Kallman's disease;
XX      KW autoimmune disease; inflammatory disease; infertility; receptor;
XX      KW acquired immune deficiency syndrome; AIDS; rheumatoid arthritis;
XX      KW allergy; osteoarthritis; diabetes mellitus; multiple sclerosis;
XX      KW systemic lupus erythematosus; cell proliferative disorder;
XX      KW cancer; developmental disorder; Duchenne muscular dystrophy; gene;
XX      KW Becker muscular dystrophy; neurological disorder; epilepsy; receptor;
XX      KW Alzheimer's disease; Huntington's disease; reproductive disorder; SS.
XX
XX      Homo sapiens.
XX
XX      Key Location/Qualifiers
XX      CDS 1..2085
XX      FT /+tag= a
XX      FT /product= "REPTR6 protein"
XX
XX      WO200198354-A2.
XX
XX      27-DEC-2001.
XX
XX      21-JUN-2001; 2001WO-US19942.
XX
XX      21-JUN-2000; 2000US-214027P.
XX      25-AUG-2000; 2000US-228045P.
XX      12-DEC-2000; 2000US-255104P.
XX
XX      (INCY-) INCYTE GENOMICS INC.
XX
XX      Griffin JA, Kallick DA, Tribouley CM, Yue H, Nguyen DB, Tang YT,
XX      Lal P, Policky JU, Azimzai Y, Lu DM, Graul R, Yao MG, Burford N;
XX      Hafalia Aduh, Baughn MR, Bandman O, Paterson C, Yang J,
XX      Gandhi AR, Warren BA, Ding L, Sanjanwala MS, Dugan BM, Lu Y;
XX

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CC identified in Drosophila, mouse, human and Caenorhabditis (see
 CC AAT89885-92) and are considered to be Wnt receptors. Wnt receptors
 CC can be used in a novel, claimed method of screening for compounds
 CC which modulate the binding of a Wnt polypeptide (secreted proteins
 CC involved in cell-to-cell signalling) to a Wnt receptor. Wnt is
 CC involved in (mammary) cancer and other processes involving growth,
 CC development and proliferation (both normal and abnormal).
 CC Modulators identified by the claimed method are useful for
 CC treatment of diseases related to these conditions.

XX
 XX Sequence 2421 BP; 403 A; 772 C; 779 G; 467 T; 0 other;

Alignment Scores:

Pred. No.:	Length:	2421
Score: 2.15e-49	Matches: 159	
Percent Similarity: 69.06%	Conservative: 24	
Best Local Similarity: 60.00%	Mismatches: 39	
Query Match: 62.86%	Indels: 43	
DB: 18	Gaps: 8	

US-09-847-102a-68 (1-235) x AAT89892 (1-2421)

```

QY 11 SerLeuLeu-----leuLeuLeuAaGlnLeuValGlyArgAlaAlaAlaSer 28
DB 218 TGGCTCTAGCCGCGCTTGGCGGTGTACAGCGCTTACGCGCGCTTCCGCGGCTTGGGCC 277
QY 29 LysAlaProValCysGlnGluIleThrValProMetCysArgGlyIleGlyTyrAsnLeu 48
DB 278 AAGGAGCTGGCGCGCCAGAGATCAGCGTGCCTTGTGCAAGCATCGGTTCACATC 337
QY 49 ThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGlnAlaGlyLeuGluValHis 68
DB 338 ACTTACATGCCCAACCAAGTTCAACGACGACCAAGATGAGCGCGCTTACGAGTGCAC 397
QY 69 GlnPheThrProLeuValGluIleGlnCysSerProAspLeuAspPhePheLeuCysTrp 88
DB 398 CAGTTTGGCGGTGTGAGATACAGTGTCTCCCGGACTCAAGTTCTTGTGTAGC 457
QY 89 MetTyrThrProIleCysLeuProAspTyrHisLysProLeuProCysArgSerVal 108
DB 458 ATGTACAGCCCATCTGCTGTGAGGACTACAGACCTTGCCTTGTGCTGTG 517
QY 109 CysGluArgAlaLysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpPro 128
DB 518 TGTGAACGGCCCAAGCGCGCTGCGCGCTCATCGCCAGTACGCGCTTGTGCTG 577
QY 129 GluArgMetSerCysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMet 148
DB 578 GACCGCATGCGCTGCATCGTGTGCGGAGCAGGCGC--AACCGGACACTGTGTGATG 634
QY 149 AspTyrAsnArgSerGluAlaThrThrAla-----ProProArgProPheProAla 165
DB 635 GACTACAAACCGACCGACCTCACCACGCGCGCCGACCGCCGCGCGCTTCCG 694
QY 166 LysProThrLeuProGly-----ProProGly 174
DB 695 CCGCCTCTCT---CCCGGAGCAGCGCGCTTGTGAGCGGCGCACAGCGCGCGCAGG 751
QY 175 Ala----- 175
DB 752 GCCAGGCCCCCATCTGTGCGGCGCAGTACGAGGCGGAGCGCGGCGGCTGCGCCC 811
QY 176 ProAlaSerGlyGlyGlyCys-----ProAlaGlyGlyProPheVal----- 189
DB 812 CCTTCGCGGCGGCGGAGGCGAGCGCCCTGTGTGCGGCGCTCTCCCTGCGAGCGGGG 871
QY 190 CysLysCysArgGluProPheValProIleLeuLysGluSerHisProLeuTyrAsnLys 209
DB 872 TGCACATGCGCGCGCCCATGTGTGAGCGGTGTCCAGGAAAGCAGCCCGCTTACACCCG 931
QY 210 ValArgThrGlyGlnAlaProAsnCysAlaValProCysTyrGlnProSerPheSerAla 229
DB 932 GTTCAGACGGCGCGCATGTGTGCGCTGCTGTGCGCACAACTTCTTTAGCCAG 991

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QY 230 AspGluArgThrPhe 234
 DB 992 GATGAGCGCGGCTTCC 1006

RESULT 4

ID ABL83141 standard; cDNA; 424 BP.

AC ABL83141;

DT 17-MAY-2002 (first entry)

XX Human ovarian cancer related cDNA clone SEQ ID NO:6119.

DE Human ovarian cancer; ovarian tumour; cytostatic; gene; ss.

XX Homo sapiens.

XX WO200192581-A2.

PN 06-DEC-2001.

PD 29-MAY-2001; 2001WO-US17756.

XX 26-MAY-2000; 2000US-207484P.

PR (CORI-) CORIXA CORP.

XX Algate PA, Harlocker SL, Jones R;

XX WPI; 2002-122075/16.

PT Composition for therapy and diagnosis of ovarian cancer comprising

PT polypeptide of a ovarian tumor polypeptide; polynucleotide encoding

PT polypeptide, antibody specific to polypeptide or T cell expressing

PT polypeptide

XX Claim 1; SEQ ID 6119; 489bp; English.

XX The present invention describes a composition (I) comprising: carriers

CC and immunostimulants; and a polypeptide (II) of a ovarian tumour

CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence

CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to

CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell

CC population of (III), or antigen-presenting cells that express (II).

CC (II) has cytosolic activity. An oligonucleotide (IV) that hybridises to

CC (S1) can be used for detecting ovarian cancer in a patient's biological

CC sample preferably serum or ovarian tissue. The method comprises

CC contacting a biological sample from a patient with (IV), detecting the

CC amount of polynucleotide hybridising to (IV) and comparing the amount to

CC a predetermined cutoff value and thereby detecting ovarian cancer in the

CC patient, where the amount of polynucleotide hybridising to (IV) is

CC detected preferably by polymerase chain reaction (PCR). (I) comprising

CC (III) and/or (II) is useful for stimulating and/or expanding T cells

CC specific for an ovarian tumour protein comprising contacting T cells

CC with (III) or (II). (III) is useful in design and preparation of

CC ribozyme molecules for inhibiting expression of the tumour polypeptides

CC and proteins in tumour cells; and to isolate a full length gene from a

CC suitable library e.g., a tumour cDNA library using well known

CC techniques.

XX Sequence 424 BP; 71 A; 163 C; 123 G; 67 T; 0 other;

Alignment Scores:

Pred. No.:	Length:	424
Score: 2.63e-45	Matches: 137	
Percent Similarity: 97.87%	Conservative: 1	
Best Local Similarity: 97.16%	Mismatches: 3	
Query Match: 57.56%	Indels: 1	
DB: 24	Gaps: 0	

US-09-847-102a-68 (1-235) x ABL83141 (1-424)

Db	874	CAGAGATGCCCGCGTCCAAACTCGGCACACCGTCGAGAGGSGCCCTTCTTACGACAC	9333
Oy	230	AspGluArgThrPheAla 235	
Db	934	GACCAAAAGGATTTCCGC 951	
RESULT 6			
AAAT89885			
ID	AAAT89885	standard; DNA; 2344 BP.	
XX	AAAT89885;		
AC			
XX			
DT	27-APR-1998	(first entry)	
DE	Drosophila frizzled gene 2 (Dfz2) encoding a Wnt receptor.		
XX			
XX	Wnt receptor; Drosophila frizzled gene 2; Dfz2 gene;		
KW	wingless receptor; Wg receptor; signal transduction; cancer;		
KM	cell growth; cell proliferation; mammary tumour; oncogene; ds.		
XX			
OS	Drosophila melanogaster.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	146..2228	
FT		/*tag= a	
FT		/transl_except= (pos:944..946, aa:Gln)	
FT		/transl_except= (pos:947..949, aa:Leu)	
FT		/transl_except= (pos:1188..1189, aa:Xaa)	
FT		/note= "this codon has an apparent 1 nucleotide deletion, which alters the reading frame"	
FT		/transl_except= (pos:1609..1611, aa:Phe)	
FT		/transl_except= (pos:2028..2040, aa:Ala)	
FT		/transl_except= (pos:2041..2043, aa:Leu)	
FT		/transl_except= (pos:2155..2156, aa:Ala)	
FT		/note= "this codon has an apparent 1 nucleotide deletion, which alters the reading frame"	
XX			
XX	MO9739357-A1.		
XX			
PD	23-OCT-1997.		
XX			
PF	11-APR-1997;	97WO-US06049.	
XX			
PR	12-APR-1996;	96US-0015307.	
XX			
PA	(UYJO) UNIV JOHNS HOPKINS.		
PA	(STRD) UNIV LELAND STANFORD JUNIOR.		
XX			
PI	Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J;		
PI	Nusse R, Samos CH, Wangy;		
XX			
DR	WPI; 1997-526631/48.		
DR	P-PSDB; AAW31267.		
PT			
PT	Identification of Wnt receptor binding modulators - useful for		
PT	treatment of cancer and growth, development or proliferation related		
PT	disorders		
XX			
XX			
PS	Disclosure; Page 21-23; 61pp; English.		
XX			
CC	This sequence comprises the Drosophila frizzled gene 2 (Dfz2) that		
CC	was identified as a receptor for wingless (Wg). To isolate the		
CC	gene, degenerate PCR primers based on sequences (see AAW31275-76)		
CC	conserved in Dfz1, human frizzled 3 (Hfz3), rat frizzled 1 (Rfz1)		
CC	and rat frizzled 2 (Rfz2) were used to amplify genomic DNA, and the		
CC	PCR product was used to isolate genomic clones of Dfz2 from an adult		
CC	Drosophila genomic library. The Drosophila frizzled-2 protein (see		
CC	AAW31267) acts as a signal transducing molecule for Wg, consistent		
CC	with its being a receptor for Wg, and is an example of a Wnt		
CC	receptor (WntR). Other novel frizzled family members have been		
CC	identified in human, mouse and Caenorhabditis elegans (see		
CC	AAH89886-92) and are also considered to be Wnt receptors. Wnt		

	<p>receptor can be used in a novel, claimed method of screening for compounds which modulate the binding of a Mnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Mnt receptor. Mnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). CC Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.</p>					
XX	Sequence 2344 BP; 469 A; 732 C; 705 G; 438 T; 0 other;					
SQ	Alignment Scores:					
	Pred. No.: 4,87e-35	Length: 2344				
OY	Score: 621.00	Matches: 124				
Db	Percent Similarity: 52.80%	Conservative: 27				
	Best Local Similarity: 43.36%	Mismatches: 55				
	Query Match: 47.40%	Gaps: 80				
	DB: 18	Gaps: 7				
US-09-847-102A-68 (1-235) x AAT89885 (1-2344)						
OY	22 GLYArgAlaAlaAlaSerLYalPro-----	31				
Db	263 GGTCAAGCGCTGACGGAGATCCCGCACCCGGTTACGAGATGCAGCCATACCAAGAT	322				
OY	32 -----ValCysgIngluileThVAlPrometCysArgGLylleGLTYrAsnIeu	48				
Db	323 CCCAATTGCCGATCGAGAGATACCACTCAATATGTCCGGCATTTGGCTTACAATG	382				
OY	49 ThrHisMetProEnglnPheAsnHIsAspThrGlnAspGluAglyLeuGluValHis	68				
Db	383 ACATTCCTTCCCACGAATAACATCATGAGACCAGAGACGAAGCGGCTGAGAGTGAC	442				
OY	69 GlnPheTrpProLeuValGluileGlnCysSerProAspLeuArgPheLeucysThr	88				
Db	443 CAGTTCTGGCCCCCTGGTGGAGATCAAAATGCTCGCGGACCTCAAGTTCTTCTTGACAGC	502				
OY	89 MetIyrThrProIleCysIeuProAspThrHisLysProIeuPropoCysArgSerVal	108				
Db	503 ATGTACACGCCCATCTGCTGAGAGATTAACACAAAGCGCTGCCGTTGCCGAGHTGC	562				
OY	109 CysGluArgAlaIalysAlaGlyCysSerProIeuMetArgInTyrglyPheAlaTrpPro	128				
Db	563 TGCGAGAGAGCGCGCTGGATGGCAACCATCATGACGACATACGTTGGAATGGCCG	622				
OY	129 GluArgMetSerCysAspArgLeuProValIleuGlyArgAspAlaGluValLeucysMet	148				
Db	623 GAGAGAATGGCGTCCGAGACACTTCCCTTCATGT---GACCCCGCAATCTGTGCATG	679				
OY	149 AspIyr-----	150				
Db	680 GAACAGCCCTGTGACAGGAGCTGGACCGGTGGACACTGGGCGGATCGGTRGCTCT	739				
OY	150 -----	150				
Db	740 GGACAGCGTTCCGCTCCGGCGGAACGAGAACGAGAGAGGACATGGCTCGGCGGACGT	799				
OY	151 -----AsnaArgSerGluAlaThrThraIaProPoaArgProPheProAlaLys	166				
Db	800 GGGGCGGCGGACGAGCGGTTTCACTCAACGAAAGCGTGCCGCGGACGCAATTCAA	859				
OY	167 ProThrIeuProGlyProProGlyAlaProAlaSerGlyGlyGlyCysProlaGlyLy	186				
Db	860 ---AActGCCMAATCCCAAGGAGAAAAGGCAAGCGGAAAAAGATGACG-----	907				
OY	187 ProPheValCysLysCysArgGluProPheVal-----	197				
Db	908 -----TCTCTGTGCGCTCCCACTCATCTTCTTCTGGGGAAGGACACTGGCTGAC	958				
OY	198 -----ProIleuLysGluSerHisProLeuTyfAsnLysVal-----	210				
Db	959 CAGCAGTGCAGATGCCCATATGACACATCACACCACTGTTACATGAACCTCATCTGT	1018				
OY	211 ---AtgThrGlyIeuValProAsnCyeAlaValProCysTyfTyrlinProSerPheSerLa	229				

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Db      1019 CAAAGATCGCCGGCTTCAACTGCGCATATCGTCAAGGGCCCTTTTCAGCAAC 1078
Qy      230 AepgluArgThrPheAla 235
Db      1079 GACGAAAGGATTTGCC 1096

RESULT 7
ID      ABL29960
ID      ABL29960 standard; DNA; 4085 BP.
XX      ABL29960;
AC      ABL29960;
DT      26-MAR-2002 (first entry)
DE      Drosophila melanogaster genomic polynucleotide SEQ ID NO 41353.
XX      Drosophila: developmental biology; cell signalling; insecticide;
KW      pharmaceutical; gene; ds.
XX      Drosophila melanogaster.
OS      Drosophila melanogaster.
FN      MO200171042-AZ.
XX      27-SEP-2001.
XX      23-MAR-2001; 2001WO-US09231.
XX      23-MAR-2000; 2000US-191637P.
PR      11-JUL-2000; 2000US-0614150.
XX      (PEKE ) PE CORP NY.
XX      Venter JC, Adams M, Li PWD, Myers EW;
XX      WPI; 2001-656860/75.
XX      New isolated nucleic acid detection reagent for detecting 1000 or more
PT      genes from Drosophila and for elucidating cell signalling and cell-cell
PT      interactions -
XX      Claim 1; SEQ ID NO 41353; 21pp + Sequence Listing; English.
XX      The invention relates to an isolated nucleic acid detection reagent
CC      capable of detecting 1000 or more genes from Drosophila. The invention is
CC      useful in developmental biology and in elucidating cell signalling and
CC      cell-cell interactions in higher eukaryotes for the development of
CC      insecticides, therapeutics and pharmaceutical drugs. The invention
CC      discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC      sequences (ABBS7737-ABBS72072).
CC      (ABBS7737-ABBS72072).
CC      The sequence data for this patent did not form part of the printed
CC      specification, but was obtained in electronic format directly from WIPO
CC      at ftp.wipo.int/pub/published_pct_sequences.
XX      Sequence 4085 BP; 949 A; 1122 C; 1102 G; 912 T; 0 other;
SQ

Alignment Scores:
Pred. No.:      9,056-35      Length:      4085
Score:          621.00      Matches:      124
Percent Similarity: 52.80%      Conservative: 27
Best Local Similarity: 43.36%      Mismatches:  55
Query Match:    47.40%      Indels:      80
DB:            23      Gaps:          7

US-09-847-102a-68 (1-235) x ABL29960 (1-4085)
Qy      22 GlyArgAlaAlaAlaSerIysAlaPro-----31
Db      1118 GGTCAAGCGCTGAGCGGATCCCGGTTACGAGTCCAGTACATACCAAGAT 1177
Qy      32 -----ValCysGlnGluIleThrValProMetCysArgGlyTlleGlyTyrIleuLeu 48

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Db      1178 CCAATCTGCATGCGAGAGATACCATACCAATGTCTCGGGCATTTGCTACACATG 1237
Qy      49 ThrHisMetProAsnGlnPheAsnHisAspThrGlnAepGluAlaGlyLeuGluValHis 68
Db      1238 ACATCTCTCCCAACGAATGAACCATGAGACCCAGAGAGGAGCGGCTGGAGGTGCAC 1297
Qy      69 GlnPheTrpProLeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThr 88
Db      1298 CAGTTCTGCCCCCTGTGTGAGATCAAAATGCTGCGGACCTCAAGTTCTTCTTCTGAGAC 1357
Qy      89 MetTyrThrProIleCysLeuProAspTyrHisIysPheProLeuProCysArgSerVal 108
Db      1358 ATGTACACGCCCATCTGCTGAGAGATTACCAACAGCCGCTGCTTTCGCGAGTGC 1417
Qy      109 CysGluArgAlaIysAlaGlyCysSerProLeuMetArgIleTyrGlyPheAlaTrpPro 128
Db      1418 TCGGAGAGAGCCCGCTCGGATGCGACCCATCATGACAGTACAGCTTGCAATGGCCG 1477
Qy      129 GluArgMetSerCysAspArgLeuProValIleuGlyArgAspAlaGluValLeuCysMet 148
Db      1478 GAGAGAAATGCGGTGAGACACTGCTCTTCATGATG--GACCCGACAATCTGTGATG 1534
Qy      149 AspTyr-----150
Db      1535 GAACAGCCCTCTGATACAGAGAGCTGGCAGCGGTGACGCTGGCGGATCGGGTGTCT 1594
Qy      150 -----150
Db      1595 GGCAGCGTTCCGGCTCCGGGGGCAACGGAAGAGGACATGCTCGGCGCGCACT 1654
Qy      151 -----AsnArgSerGluAlaThrThraIaProProArgProPheProAlaIys 166
Db      1655 GGGCGCGGAGCAGAGCGGTTCCACTCAACAGAGCCGTGCGCGGAGCAGCAATTCAAA 1714
Qy      167 ProThrLeuProGlyProProGlyAlaProAlaSerGlyGlyGluCysProAlaIleGly 186
Db      1715 --AATGCCAAMATCCCAAGAGAAAGCAAGCGGAAAGAGTGCAGC-----1762
Qy      187 ProPheValCysIysCysArgGluProPheVal-----197
Db      1763 -----TCTGTGCTGCTCCCTCCCACTCATCTTCTCTGGGAGAGACAGCTGCTGAG 1813
Qy      198 -----ProIleuIysGluSerHisProLeuTyrAsnIysVal-----210
Db      1814 CAGAGTGCAGATGCCATGATGACATCATCACACCACTGATCATGACCTCACTGTC 1873
Qy      211 ---ArgThrIysGlnValProAsnCysAlaValProCysTyrGlnProSerPheSerAla 229
Db      1874 CAAAGGATCGCGCGCTTCCAAACTGCGCATACCGTCAAGGGCCCTTCTTCAGCAAC 1933
Qy      230 AepgluArgThrPheAla 235
Db      1934 GACGAAAGGATTTGCC 1951

RESULT 8
ID      AAT89891
ID      AAT89891 standard; DNA; 2259 BP.
XX      AAT89891;
XX      27-APR-1998 (first entry)
DE      Mouse frizzled gene 7 (Mfz7) encoding a Wnt receptor.
XX      Wnt receptor; mouse frizzled gene 7; Mfz7 gene;
KW      signal transduction; cancer; cell growth; cell proliferation;
KW      mammary tumour; oncogene; therapy; ds.
XX      Mus musculus.
OS      Mus musculus.
FH      Key
FT      CDS      Location/Qualifiers
FT      361..2079
FT      /*tag= a

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P5 Claim 3; Page 192-193; 410pp; English.
 XX Secretory proteins play important roles in the proliferation control, the
 CC differentiation induction, the material transport and the biophylaxis of
 CC cells. Membrane proteins have important roles as signal receptors, ion
 CC channels and transporters. The present sequence is the coding sequence
 CC for a human protein which has at least one hydrophobic domain. The
 CC protein encoded by the present sequence may be a secretory or a membrane
 CC protein. The encoded protein may have cytokine and cell
 CC proliferation/differentiation activity, immune stimulating or suppressing
 CC activity, haematopoiesis activity, tissue growth activity, haemostatic
 CC and thrombolytic activity, anti-inflammatory activity and tumour
 CC inhibition activity. The present sequence could therefore be used for
 CC treatment of autoimmune disease, Alzheimer's disease, Parkinson's
 CC disease, and cancer via gene therapy.

SQ Sequence 1941 BP, 317 A; 642 C; 629 G; 353 T; 0 other;

Alignment Scores:

Pred. No.:	1,64e-20	Length:	1941
Score:	415.00	Matches:	104
Percent Similarity:	46.37%	Conservative:	30
Best Local Similarity:	35.99%	Mismatches:	87
Query Match:	31.68%	Indels:	68
DB:	21	Gaps:	11

US-09-847-102a-68 (1-235) x AAA60179 (1-1941)

QY 3 ArgPro-----AspProSerAlaProProSerLeuLeuLeuLeu----- 17
 DB 127 GCGCCGCCAGTTGACCCCGCGGATGCGCGCCAGCTCTCTCTGTTGGCTGCTG 186
 QY 18 -----AlaGlnLeuValGly---ArgAlaAlaAlaSerLeuAlaPro----- 31
 DB 187 GAGGCTCCGCTCTGCTGCGGGGTCCGAGCCAGCGCGCGGCGGCGGCGGCGG 246
 QY 31 ----- 31
 DB 247 CCGGGCGCGGCGGAGCAACCGCGCGCGCTCAGCAGCAACAGCGGCGGCGAGTAC 306
 QY 32 -----ValGlyGlnGlnLeuValPro 39
 DB 307 AACGGCAGCGGCGGATCTCCGCGGACACAGCGGTATGCGAGCCCATCTCCG 366
 QY 40 MetCysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThr 59
 DB 367 CTGTGACGACATGCGGTACAAACAGACCATCATGCCCCAACCTGCGGCGCACGAA 426
 QY 60 GlnAspGlnAlaGlyLeuGlnValHisGlnPheTyrProLeuValGlnIleCysSer 79
 DB 427 CAGAGAGACGCGGCGGCTGAGGTGACACGCTTCTACCTCTGTAAGTACAGTCTCC 486
 QY 80 ProAspLeuArgPhePheLeuCysThrMetTyrThrProIleCysLeuProAspTyrHis 99
 DB 487 GCTGAGCTCAAGTCTCTCTGCTCTCATGTACGCGCCGCTGACCGCTG---CTAGAG 543
 QY 100 LysProLeuProProCysArgSerValCysGlnArgAlaAlaGlyCysSerProLeu 119
 DB 544 CAGGGCGTGCCTCCGCGCTCCGTCGAGCGCGCGCGGCGGCGGCGGCGGCGCTC 603
 QY 120 MetArgGlnTyrGlyPheAlaTyrProGlnArgMetSerCysAspArgLeuProValLeu 139
 DB 604 ATGAACAAGATTGCGGCTTCCAGTGGCCAGACAGCTCAAGTGTGAGAGATCCCGGCGAC 663
 QY 140 GlyArgAspAlaGlnValLeuCysMetAspTyrAsnArgSerGlnAlaThrThralPro 159
 DB 664 GGC-----GCCGCGAGCTGTGCGTGGCCAGAACCTCCGACAGGCGCCGACG 717
 QY 160 ProArgProPheProAlaLysProThrLysProGlyProProGlyValAlaProLaserGly 179
 DB 718 CCTGCTGCTCTTCCAGAGTCTTGACACCAACCTCAGACGCGCGGCGGAGGCGACCGT 777

QY 180 GlyIleCysProAlaGly-----GlyProPheValCysLeuCysArg 193
 DB 778 GCGCGCTCTCCGCGGCGGCGCGCGCGCTGCGAGCAGGCAAGTCTCTGCGCCG---GCG 834
 QY 194 GlnProPheValProIleLeuLysGlnSerHisProLeuTyrAsnLeuValArgThrGly 213
 DB 835 GCCCTCAAGGTGCTCTCTTACTCACTACCACTCACTCTGCGGAGAG----- 882
 QY 214 GlnValProAsnCysAlaValAlaProCysTyrGlnProSer----- 226
 DB 883 -----GACTGCGGCGCACCTTGT---GAGCCGACCAAGGTATGAGCTCATGTAC 930
 QY 227 PheSerAlaAspGlnArgThrPheAla 235
 DB 931 TTCGGCGCCGAGAGACTGCGCTTCTCG 957
 RESULT 10
 AAA60189
 ID AAA60189 standard; DNA; 4485 BP.
 XX
 AC AAA60189;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE Hydrophobic domain protein cDNA HP02539 isolated from Saos-2 cells.
 XX
 KW Human; secreted protein; membrane protein; hydrophobic domain;
 KW proliferation control; differentiation induction; material transport;
 KW biophylaxis; signal receptor; ion channel; transporter; immunostimulant;
 KW immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic;
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
 KW autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer;
 KW gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO20029448-A2.
 XX
 PD 25-MAY-2000.
 XX
 PF 17-NOV-1999; 99WO-UP06412.
 XX
 PR 17-NOV-1998; 98JP-0326255.
 XX
 PR 22-DEC-1998; 98JP-0364315.
 XX
 PR 16-MAR-1999; 99JP-0069811.
 XX
 PR 27-APR-1999; 98JP-0192299.
 XX
 PR 19-MAY-1999; 99JP-0138169.
 XX
 PA (SAGA) SAGAMI CHEM RES CENT.
 PA (PROT-) PROTEGENE INC.
 XX
 PI Kato S, Kimura T;
 XX
 DR WPI; 2000-387753/33.
 DR P-PSDB; AAB12117.
 XX
 PT Proteins comprising hydrophobic regions, such as secretory and membrane
 PT proteins, useful in research and diagnostics and having various
 PT activities e.g. immunomodulatory, anti-inflammatory, chemokinetic,
 PT hemostatic, thrombolytic -
 XX
 PS Claim 4; Page 199-204; 410pp; English.
 XX
 CC Secretory proteins play important roles in the proliferation control, the
 CC differentiation induction, the material transport and the biophylaxis of
 CC cells. Membrane proteins have important roles as signal receptors, ion
 CC channels and transporters. The present sequence is the coding sequence
 CC for a human protein which has at least one hydrophobic domain. The
 CC protein encoded by the present sequence may be a secretory or a membrane
 CC protein. The encoded protein may have cytokine and cell
 CC proliferation/differentiation activity, immune stimulating or suppressing
 CC activity, haematopoiesis activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, anti-inflammatory activity and tumour
inhibition activity. The present sequence could therefore be used for
treatment of autoimmune disease, Alzheimer's disease, Parkinson's
disease, and cancer via gene therapy.

XX Sequence 4485 BP; 1002 A; 1198 C; 1193 G; 1092 T; 0 other;

Alignment Scores:

Pred. No.:	4.17e-20	Length:	4485
Score:	415.00	Matches:	104
Percent Similarity:	46.37%	Conservative:	30
Best Local Similarity:	35.99%	Mismatches:	87
Query Match:	31.68%	Indels:	68
DB:	21	Gaps:	11

US-09-847-102a-68 (1-235) x AAA60189 (1-4485)

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QY 3 ArgPro-----AsProSerAlaProProSerLeuLeuLeuLeuLeu----- 17
    |||||
DB 315 CCGCCCGCAGATTGACCCCGCGCGATTGGCGCGCCACCTGCTGCTGCTTGGCTGCTG 374
    |||||
QY 18 -----AlaGlnLeuValGly---ArgAlaAlaAlaAlaSerIysAlaPro----- 31
    |||||
DB 375 GAGGCTCCGCTGCTGCTGGGGGCTCCGGGCCAGCGCGCGCCAGGCGCCAGGCGGAG 434
    |||||
QY 31 ----- 31
DB 435 CCGCGCGCGGCGAGCAGACCGCGCGCGCTCAGCAGACAGCGCGGCGAGCAGTAC 494
    |||||
QY 32 -----ValCysGlnGlnLeuLeuValPro 39
DB 495 AACGGGAGCGGGGAGCTCCCGTCCCGGACACAGCGGTATTGGCCAGCCATCTCCATCCG 554
    |||||
QY 40 MetCysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnIleAsnHisAspThr 59
    |||||
DB 555 CTGTGACGAGCATCTCCGTCACACAGACCATATATGCTCCACTGCTGGGCCACAGAAC 614
    |||||
QY 60 GlnAspGlnAlaGlyLeuGlnValHisGlnIlePheTyrProLeuValGlnIleGlnCysSer 79
    |||||
DB 615 CAGAGACGCGCGGCGCTGAGGTGACCACTTCTACCTCTAGTGAAGTGAAGTGTTC 674
    |||||
QY 80 ProAspLeuArgPhePheLeuLeuCysThrMetTyrThrProIleCysLeuProAspTyrHis 99
    |||||
DB 675 GCTGACTCAAGTCTTCTGTCCTGTCATGTACGCCCGCTGTGACCCGCGT--CTAGAG 731
    |||||
QY 100 LysProLeuProProCysArgSerValCysGlnArgAlaLysAlaGlyCysSerProLeu 119
    |||||
DB 732 CAGGCGCTGCGCGCTGCGCTCTCTGTGAGCGCGCGCGCGCGCGCGCGCGCTC 791
    |||||
QY 120 MetArgGlnTyrGlyPheAlaTyrProGlnArgMetSerCysAspArgLeuProValLeu 139
    |||||
DB 792 ATGAACAAAGTGGCTTCCAGTGGCCAGACAGCTCAAGTGAAGTTCGCGGTGCAC 851
    |||||
QY 140 GlyArgAspAlaGlnValLeuLeuCysMetAspTyrAsnArgSerGlnAlaThrThrAlaPro 159
    |||||
DB 852 GGC-----GCCGGCAGAGCTGTGCGGGCCAGAACAGCTCCACAGAGGCGCCGACG 905
    |||||
QY 160 ProArgProPheProAlaLysProThrLeuProGlyProProGlyAlaProAlaSerGly 179
    |||||
DB 906 CCTCGCTGCTTCAAGTTCCTGACACGACACCTCAGACGCGCGCGGAGGCGACCGT 965
    |||||
QY 180 GlnGluCysProAlaGly-----GlyProPheValCysIysCysArg 193
    |||||
DB 966 GGGGGCTCCCGGGGGCGCGCGCGCGCGCGAGCGAGCGAGGAAAGTTCGCGCGCG 1022
    |||||
QY 194 GluProPheValProIleLeuLysGlnSerHisProLeuTyrAsnLysValArgThrGly 213
    |||||
DB 1023 GCCCTCAAGTGCCTTCACTCACTCACTCACTTCTTGGGAGAG----- 1070
    |||||
QY 214 GlnValProAsnCysAlaValProCysTyrGlnProSer----- 226
    |||||
DB 1071 -----GACTGCGGCGCAGCTTGT---GAGCCGACCAAGGTGATGGCTCATGTAC 1118
    |||||

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QY 227 PheSerAlaAspGlnArgThrPheAla 235
DB 1119 TTCGGGCCGAGAGAGCTGCGCTTTCG 1145

RESULT 11

ID ABK63777 standard, cDNA, 4540 BP.

XX ABK63777;

DT 18-JUN-2002 (first entry)

DE Rat sequence differentially expressed in response to a hepatotoxin #1684.

KW Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;

XX differential expression; centrilobular necrosis; steatosis.

OS Rattus norvegicus.

PN WO200210453-A2.

PD 07-FEB-2002.

PF 30-JUL-2001; 2001WO-US23872.

XX 31-JUL-2000; 2000US-222040P.

PR 02-NOV-2000; 2000US-244880P.

PR 11-MAY-2001; 2001US-290029P.

PR 15-MAY-2001; 2001US-290645P.

PR 22-MAY-2001; 2001US-292336P.

PR 06-JUN-2001; 2001US-295798P.

PR 13-JUN-2001; 2001US-297457P.

PR 19-JUN-2001; 2001US-298884P.

PR 09-JUL-2001; 2001US-303459P.

XX (GENE-) GENE LOGIC INC.

XX Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;

XX WPI; 2002-241625/29.

XX Predicting toxic effects of compounds or the progression of these toxic

PT effects by determining the changes in gene expression in tissues or

PT cells exposed to the toxin and comparing these to gene expression in

PT unexposed tissues or cells -

XX Claim 1; Seq ID No 1684; 239pp; English.

XX The invention relates to methods for predicting toxic effects of

XX compounds or the progression of these toxic effects by determining the

XX global changes in gene expression in tissues or cells exposed to the

XX toxin and comparing these to gene expression in unexposed tissues or

XX cells. Also included are methods of predicting at least one toxic

XX effect of a compound or progression of a toxic effect, preferably the

XX hepatotoxicity of a compound, comprising detecting the level of

XX expression in a tissue or cell sample exposed to the compound of two or

XX more genes listed in the specification, where differential expression of

XX the genes is indicative of at least one toxic effect or progression.

XX The method can also be used to identify an agent which modulates the

XX toxic response and predict cellular pathways that a compound modulates

XX in a cell. The methods utilize a set of at least two probes (on a solid

XX support in kit form), where each of the probes comprises a sequence that

XX specifically hybridises to a gene listed in the specification, a computer

XX system comprising a database containing information identifying the

XX expression level in a tissue or cell sample exposed to a hepatotoxin of a

XX set of genes comprising at least two genes listed in the specification,

XX and a user interface to view the information used to present information

XX identifying the expression level in a tissue or cell of at least one gene

XX listed in the specification. The method is useful for elucidating global

XX changes in gene expression and for identifying toxicity markers in

XX tissues or cell exposed to a known toxin. The genes may be used as

XX toxicity markers in drug screening and toxicity assays. The genes and

XX gene expression information may be used as diagnostic markers for the

CC prediction or identification of the physiological state of tissue or cell
CC sample that has been exposed to a compound or agent. Hepatotoxicity
CC is characterised by centrilobular necrosis and steatosis. The present
CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
CC which is differentially expressed in response to a hepatotoxic agent.
CV

SQ Sequence 4540 BP; 998 A; 1255 C; 1220 G; 1067 T; 0 other;

Alignment Scores:

Pred. No.:	6, 8e-19	Length:	4540
Score:	398.00	Matches:	88
Percent Similarity:	53.708	Conservative:	28
Best Local Similarity:	40.744	Mismatches:	74
Query Match:	30.384	Indels:	26
DB:	24	Gaps:	8

US-09-847-102A-68 (1-235) X ABK63777 (1-4540)

OY	33	CysGlnGlnIuIethValProMeCysAArgGlyIleGlyTYrAsnLeuThrHiIserPro	52
Db	1096	TGTCAAGCCCATCTCCATCCCGCTGTGCACGGACATCGGCTCAATCAGACATCATGAGCC	1155
OY	53	AasnInpAasnHiAspThrGlnAspGluIleGlyLeuGluValHisGlnPheThrPro	72
Db	1156	AACCTGCTGGGACACACGATCAGAGAGACCGCGGCTTGAGAGTGCACAGATTGACCG	1215
OY	73	LeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThiMetTYrThrPro	92
Db	1216	TTGGTGAAGGTGCACTGCTCAGCCACAGTCAAGTCTTCGTGCTCATGTACCGCGCT	1275
OY	93	IleCysLeuProAspTYrHiIlyAspProLeuProProCysArgSerValCysGluIuArgIa	112
Db	1276	GTCGTCCAGGTA---CTGAGCAGAGCGCTGCTCTCCCTCCGCTCTGTGAGCGCGCC	1332
OY	113	LysAlaGlyCysSerProLeuMetArgGlnTYrGlyPheAlaTrpProGluArgMetSer	132
Db	1333	CAG---GGCTCGAGGACACTATGAAACAAGTTCGGCTTCAGATGGCCAGACACGCTCAG	1389
OY	133	CysAspArgLeuProValLeuGlyYArgAspAlaGluValLeuCysMetAspTYrAsnArg	152
Db	1390	TGCGAAGATTCCCTGTGCACGGC---GCAGAGAGCTGTGCGTGGGCCAGAACT	1443
OY	153	SerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuProGlyPro	172
Db	1444	TCCGACAAAGGACACCCGACATCCCTCCTGTCGCGGAGATTGTGACACAGAACTCCGAG	1503
OY	173	ProGlyAlaProAlaSerGlyGlyGluCysProAlaGly-----Gly	186
Db	1504	CACGGCGCGGTGATTACCGCGGCGGCTACCCGGAGAGGTGCGCGGCCCGCTGAGAGCGGA	1563
OY	187	ProPheValCysLysCysArgGluProPheValProIleLeuLysGluSerHiIserProLeu	206
Db	1564	AAGTTCTCTGCGCG---CGCGCCCTCAGGGGCTTCTTCACTCACTATCATCTTCTG	1620
OY	207	TYrAsnLysValArgThrGlyGlnValProAsnCysAlaValAlaProCysTYrGlnProSer	226
Db	1621	GGGGAGAG-----GACTCGGGCGGCGCTGC---GAACCCACT	1656
OY	227	-----PheSerAlaAspGluArgThrPheAla	235
Db	1657	AAAGTATACGGGCTCATGTACTCGGGCTGAGGAGTGGCGCTTTG	1704
RESULT 12			
AAAF75974			
ID AAF75974 standard; cDNA, 3269 BP.			
XX AAF75974;			
XX AC			
XX DT 22-MAY-2001 (first entry)			
XX Human frizzled family gene 584 cDNA.			
DE Human frizzled family gene 584 cDNA.			
KW Human; frizzled family gene 584; embryo; foetus; cancer;			

KW drug discovery; cytostatic; ss

OS Homo sapiens.

PN WO200112808-A1

PD 22-FEB-2001.

PF 18-AUG-2000; 2000WO-JP05552.

PR 18-AUG-1999; 99JP-0232018.

PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

PI Senoo C, Numata M;

DR WPI; 2001-211220/21.

XX

PT as well as in cancer cells, useful in drug development for diseases

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XX The invention relates to a novel frizzled family gene, 584, from mouse
CC and human (cDNAs given in AAF75973 and AAF75974), and to the mouse and
CC human 584 proteins (AAF7307, AAF7308). Gene 584 is strongly expressed
CC in the embryo and foetus, and is also strongly expressed in cancer
CC cells. The invention also relates to recombinant vectors and host
CC cells comprising gene 584 nucleic acids, the recombinant expression of
CC the 584 protein, methods of screening for modulators of 584 activity or
CC expression, and the compounds thus identified. The human and mouse 584
CC genes represent a novel gene target for the development of drugs useful

SQ Sequence 3269 BP; 688 A; 961 C; 941 G; 668 T; 11 other;

Alignment Scores:

Pred. No.:	2,84e+18	Length:	3265
Score:	387.00	Matches:	88
Percent Similarity:	50.88	Conservative:	28
Best Local Similarity:	38.60	Mismatches:	71
Query Match:	29.54	Indels:	42
DB:	22	Gaps:	8

US-09-847-102A-68 (1-235) X AAF75974 (1-3269)

QY	1	MethylarprobsproserhlaProproserleuLeuLeuLeuLeuLaGluLeu	20
Db	486	ATGCAGGCCCCGGCCCCCGC-----CTGGGCTGCTCTGAGGTG	52
QY	21	ValGlyARgLaLaLaLaLaSerLyalaProVal-----Cys	33
Db	528	ATGGGCTCGGCGCCCGCCATGAGCTTCATGACATGACAGCGCCGCGGACGCAAAATGC	587
QY	34	GlnGluLeuLeuPhePheMetCysARProGlyLeuGlyTyrAsnLeuLeuThiAsnMetProAsn	53
Db	588	CAGCCCATCGAATGCCCATGTGCGAAGACATCGGCTCTCAACATGATCTCGTATGCCAAC	64
QY	54	GlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrpProLeu	73
Db	648	CTGATGGGCGACAGAAACCGACGCGACGAGGAGCATCTCCAGTTCGACGAGTTGCGCCCGTG	707
QY	74	ValGluLeuLeuGlnCysSerProAspLeuARPhePheLeuCysThiMetTyrThiProLe	93
Db	708	GTCGAGTACGCGTCGCCACGCGCACTCCGCTTCTCTCTGCTCGCTCTACGCCCGCATG	76
QY	94	CysLeuProAspPtyrHisIblyProLeuProProCysValGserValCysGluARAlaIbly	113
Db	768	TGCACCGAGACAGGTCTTACCCCATTCCTCCCGCTCCGGATCATGTGGACACAGCCCG	827

PN WO200212440-A2.
 XX 14-FEB-2002.
 XX 07-AUG-2001; 2001WO-US24708.
 XX 07-AUG-2000; 2000US-22323P.
 XX 05-JUN-2001; 2001US-0873319.
 XX (GENE-) GENE LOGIC INC.
 XX (NISB) JAPAN TOBACCO INC.
 PI Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;
 DR WPI; 2002-257476/30.
 PT Identifying drugs for and diagnosing benign prostatic hyperplasia, by
 PT detecting expression levels of one or more genes in prostate cells from
 PT cells that are differentially regulated compared to normal prostate
 cells
 PS Disclosure; Page 353-354; 444pp; English.
 XX The invention relates to a method of diagnosing (I) the onset or
 CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
 CC or identifying an agent that modulates the onset or progression of BPH.
 CC The method is based on changes in gene expression in BPH tissue isolated
 CC from patients exhibiting different clinical states of prostate
 CC hyperplasia as compared to normal prostate tissue. (I) comprises
 CC detecting the expression levels of one or more genes in prostate cells
 CC from the subject that are differentially regulated compared to normal
 CC prostate cells. (II) comprises preparing a first gene expression profile
 CC of BPH cells or BPH-like cell population, exposing the cells to the
 CC agent, preparing a second gene expression profile of the agent exposed
 CC cells, and comparing the first and second gene expression profiles.
 CC (II) is useful for diagnosing the onset or progression of BPH. (II) is
 CC useful for identifying an agent that modulates the onset or progression
 CC of BPH. The methods are useful to prevent information identifying
 CC the expression level in a tissue or cells, by comparing the expression
 CC level of genes given in the specification in the tissue or cells to the
 CC level of expression of gene in the database, and displaying the
 CC expression levels of at least one gene in the tissue or cell sample
 CC compared to the expression level in BPH. Agents using (II) are useful for
 CC treating BPH or prostate cancer. ABK64106-ABK64860 represent human
 CC benign prostatic hyperplasia gene sequences of the invention.
 SQ Sequence 1909 BP; 523 A; 441 C; 437 G; 507 T; 1 other;

Alignment Scores:
 Pred. No.: 4,51e-18 Length: 1909
 Score: 380.50 Matches: 83
 Percent Similarity: 50.00% Conservative: 35
 Best Local Similarity: 35.17% Mismatches: 83
 Query Match: 29,058 Indels: 35
 DB: 24 Gaps: 8

US-09-847-102a-68 (1-235) x ABK64750 (1-1909)
 QY 4 ProAaPProSer-----AlaProProSerLeuLeuLeuLeuLeuLeuAla 18
 DB 52 CCCCACTCTGGCGGATCATGTCTGGCGGACCCGGAGGAGATCTGTGTGGCGGCC 111
 QY 19 GlnLeuValGlyArgAlaAla-----AlaAlaSerLeuValProVal 32
 DB 112 GGGCTGCTTCCCT 171
 QY 33 CysGlnGlnIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetPro 52
 DB 172 TGTGAGCCCGCTCGCATCCCTCTGTGCAAGTCCCTCTGCAATCATGATGAGCC 231
 QY 53 AaangInPheAsnHisSerPheGlnIleArgIleValGlyLeuGlnValHisGlnPheTrpPro 72
 DB 232 AACCACTGACACAGCACTAGAGCAACGCAATCTCTGCGCATGAGAGTTGAAAGT 291

QY 73 LeuValGlnIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetTyrThrPro 92
 DB 292 CTGCTGGGACCACTGACGAGCCGATCTGCTCTCTCTCTCTCTGTCATGACCGCC 351
 QY 93 IleCysLeuProAspTyr---HisLeuProLeuProProCysArgSerValCysGlnArg 111
 DB 352 ATCTGCACCATTTGATTTCTTACACGACGACCATCAAGCCCTCTTAATCTGTGTGCGAGCG 411
 QY 112 AlaValAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTyrProGlnArgMet 131
 DB 412 GCCCGGAGGCTGTGACCCCATCTACTCATCAAGTACCGCCACTGTGCGGAGAACTGT 471
 QY 132 SerCysAspArgLeuProValIleuGlyArgAspAlaGlnValLeuCysMetAspTyrAsn 151
 DB 472 GCCTCGAGGAGCTGCCAGTGTACAGACAGGGCC-----GTGTGCATC-----TCT 516
 QY 152 ArgSerGlnAlaThrThrAlaProProArgProPheProAlaValProThrLeuProGly 171
 DB 517 CCCGAGGCCATCTTACTGCGGACGACCTGATTTTCT----- 555
 QY 172 ProProGlyAlaProAlaSerGlyGlyLeuCysProAlaGlyGlyProPheValCysAsp 191
 DB 556 -----ATGATTTCTAGTACGAGAACTGTAGAGGGCGCAAGCATGACGCTGTAA 606
 QY 192 CysArgGluProPheValProIleLeuLysGlnSerHisProLeu-----Tyr 207
 DB 607 TGTAA-----CTATTAGACTACACAGAAAGACTATTCCGGAACATTAC 654
 QY 208 AsnLysValArgThrGlyGlnValProAsnCysAlaValProCysTyr 223
 DB 655 AACATGTGATTCGGGCTAAAGATTAAAGATTAAGACTAAGTGCAT 702

RESULT 15
 ID ABL61945 standard; DNA; 1909 BP.
 XX ABL61945;
 AC 15-MAY-2002 (first entry)
 DT 15-MAY-2002 (first entry)
 XX
 DE Colon adenocarcinoma related gene sequence SEQ ID NO:282.
 XX
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilms tumour; adenocarcinoma;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200194629-A2.
 PD 13-DEC-2001.
 XX
 PF 30-MAY-2001; 2001WO-US10838.
 XX
 XX 05-JUN-2000; 2000US-209473P.
 PR 05-JUN-2000; 2000US-209531P.
 PR 18-SEP-2000; 2000US-233133P.
 PR 18-SEP-2000; 2000US-233617P.
 PR 20-SEP-2000; 2000US-234009P.
 PR 20-SEP-2000; 2000US-234034P.
 PR 20-SEP-2000; 2000US-234052P.
 PR 22-SEP-2000; 2000US-234509P.
 PR 22-SEP-2000; 2000US-234567P.
 PR 22-SEP-2000; 2000US-234923P.
 PR 25-SEP-2000; 2000US-234924P.
 PR 25-SEP-2000; 2000US-235077P.
 PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 25-SEP-2000; 2000US-235280P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 26-SEP-2000; 2000US-235639P.

PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 27-SEP-2000; 2000US-235863P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236891P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.
 XX (AVAL-) AVALON PHARM.
 XX PA
 PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX WPI; 2002-188264/24.
 XX
 PT Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set
 XX
 PS Claim 1; SEQ ID 282; 44pp: English.
 XX
 CC The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL1664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytosolic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer.
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilms' tumour.
 XX
 SQ Sequence 1909 BP; 523 A; 441 C; 437 G; 507 T; 1 other;

Alignment Scores:
 Pred. No.: 4, 51e-18 Length: 1909
 Score: 380.50 Matches: 83
 Percent Similarity: 50.00% Conservative: 35
 Best Local Similarity: 35.17% Mismatches: 83
 Query Match: 29.05% Indels: 35
 DB: 24 Gaps: 8

US-09-847-102a-68 (1-235) x ABL61945 (1-1909)

QY 4 ProAspProSer-----AlaProProSerLeuLeuLeuLeuAla 18
 DB 52 CCCATCTCTGCGGAGTATGTCGTGCGGAGCCCGGAGGAGTCTGCTGCGGAGCC 111

QY 19 GlnLeuValGlyArgAlaAla-----AlaAlaSerLeuAlaProVal 32
 DB 112 GGGCTGCTTGCCCTGCTGCTCTCTGCTGCTCCGGGTGCCCCGGGCTCGGCTCAGCC 171
 QY 33 CysGlnGluIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetPro 52
 DB 172 TGTGAGCCCGTCGATCCCTCTGTGCAAGTCCCTGCGCCCTGGAGACATGATGATGCC 231
 QY 53 AsnGlnPheAsnHisAspThrGlnAspGluIleGlyLeuGluValHisGlnPheThrPro 72
 DB 232 AACCACTGCACACACAGACTCAGAGCAACGCCATCTGGCCATGAGAGATTCCAGGT 291
 QY 73 LeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThrTyrThrPro 92
 DB 292 CTGCTGGGACCACTGACAGCCCGCATCTGCTCTCTCTGTCATGATGACGCGCC 351
 QY 93 IleCysLeuProAspTyr---HisTyrProLeuProProCysArgSerValCysGluArg 111
 DB 352 ATCTGACCATTTGATTCACAGCAGCCCATCAAGCCCTGTAACTGTGTGCGAGCGG 411
 QY 112 AlaLysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArgMet 131
 DB 412 GCCCGCAGGCGCTGTGAGCCCATCTCATCAAGTACCCGCACTCGTGGCGGAGAACCTG 471
 QY 132 SerCysAspArgLeuProValIleuGlyArgAlaAlaGluValLeuCysMetAspTyrAsn 151
 DB 472 GCCTCGAGGAGACTCCAGTGTACGACAGAGGGGC-----GTGTGATC-----TCT 516
 QY 152 ArgSerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuProGly 171
 DB 517 CCCGAGGCCATCGTTACTGCGGAGCGAGCTGATTTTCT----- 555
 QY 172 ProGluValAlaProAlaSerGlyGlyGluCysProAlaGlyGlyProPheValCysLys 191
 DB 556 -----ATGCAATTCTAGTAAGCAAACTGTAGAGGGGCAAGAGAGTAAAGCTGTAA 606
 QY 192 CysArgGluProPheValProIleLeuLysGlnSerHisProLeu-----Tyr 207
 DB 607 TGTAA-----CTATTAGACTACACAGAACCTATTTCGGAACAATTAAC 654
 QY 208 AsnLysValArgThrGlyGlnValProAsnCysAlaValProCysTyr 223
 DB 655 AACATATGATTCGGGCTTAAGTTAAAGATTAAGACTTAAGTGCAT 702

Search completed: May 22, 2003, 23:39:12
 Job time : 270 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 22, 2003, 18:09:48 ; Search time 56 Seconds
(without alignments)
1286.947 Million cell updates/sec

Title: US-09-847-102a-68

Perfect score: 1310
Sequence: 1 MARPPSAPSLLLLLLAQL.....PNCAPVCYQPSFADERTFA 235

Scoring table: BLOSUM62

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Fgapop 10.0	Fgapext 0.5
Delop 6.0	Delext 7.0

Searched: 441362 segs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-O=/cg2_1/USPTO.spool/US09847102/runat.19052003.160407.744/app.query.fasta_1.391
-DB=Issued_Patents_NA -QFMT=faststep -SUFFIX=rm1 -MINMATCH=0.1 -IOFCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Database :

Issued Patents NA: *
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6: /cg2_6/pdata/1/ina/6D.COMB.seq: *

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	378	28.9	1893	3	US-08-878-474-10
2	372.5	28.4	2039	3	US-09-276-531-45
3	367	28.0	2176	3	US-08-878-474-8
4	360	27.5	1875	3	US-08-878-474-4
5	342.5	26.1	2009	4	US-09-276-531-108
6	297	22.7	1796	4	US-09-276-531-113
7	284.5	21.7	1796	4	US-09-276-531-113
8	282	21.5	2833	4	US-09-276-531-23
9	280	21.5	2880	4	US-08-987-289-1
10	274.5	21.0	1984	4	US-08-937-067-5
11	271	20.7	870	4	US-08-937-067-3
12	246	18.8	1146	4	US-08-893-654B-5

13	240.5	18.4	1308	4	US-08-937-067-18
14	240.5	18.4	4245	4	US-09-276-531-16
15	231.5	17.7	2190	4	US-08-893-654B-1
16	231	17.6	1140	4	US-08-893-654B-3
17	227.5	17.4	502	4	US-08-893-654B-7
18	142	10.8	1739	2	US-08-681-151-2
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20	139.5	10.6	2972	2	US-08-953-823A-3
21	139.5	10.6	2972	2	US-09-398-239-3
22	130	9.9	3854	2	US-08-720-484A-1
23	130	9.9	3854	2	US-08-953-823A-1
24	130	9.9	3854	2	US-09-398-239-1
25	118	9.0	34063	4	US-09-453-702B-96
26	112.5	8.6	53526	3	US-08-658-136-2
27	112.5	8.6	53527	3	US-08-658-136-1
28	111	8.5	2220	4	US-08-765-907A-14
29	110.5	8.4	4496	4	US-08-765-907A-6
30	107.5	8.2	2604	5	PCT-US95-08493-20
31	107	8.2	3901	1	US-08-188-562-31
32	107	8.2	3901	1	US-08-646-715-31
33	106	8.1	36519	3	US-08-923-137-2
34	105.5	8.1	3879	4	US-08-916-352-1
35	105.5	8.1	5836	4	US-09-453-702B-253
36	105.5	8.1	4403765	4	US-09-103-840A-2
37	105.5	8.1	4411529	4	US-09-103-840A-1
38	105	8.0	1265	1	US-08-132-649-5
39	105	8.0	1265	3	US-08-767-579-5
40	105	8.0	2430	4	US-09-232-160-16
41	103.5	7.9	48908	4	US-09-453-702B-137
42	103	7.9	3777	3	US-09-121-321-15
43	103	7.9	3777	4	US-08-933-803A-15
44	103	7.9	4403765	4	US-09-103-840A-2
45	103	7.9	4411529	4	US-09-103-840A-1

ALIGNMENTS

RESULT 1
US-08-878-474-10
Sequence 10, Application US/08878474
Patent No. 6,133,232
GENERAL INFORMATION:
APPLICANT: De Robertis, Edward M.
TITLE OF INVENTION: Endostem, Cardiac and Neural Inducing
TITLE OF INVENTION: Endostem, Cardiac and Neural Inducing
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Majestic, Parsons, Siebert & Huse
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878, 474
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,150
FILING DATE: 20-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 3100.002US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/248-5500
TELEFAX: 415/362-5418

```

; INFORMATION FOR SEQ ID NO: 10
;
; SEQUENCE CHARACTERISTICS:
;
;   LENGTH: 1893 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;
;   MOLECULE TYPE: cdna
;
US-08-878-474-10

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[illegible]

US-09-847-102A-68 (1-235) x US-08-878-474-10 (1-1893)

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Oy	18	Ala	gln	Val	Gly	Arg	Ala	Ala	-----	Ala	Asp	31	
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Oy	32	Val	Cys	gln	gln	Ile	Thr	Val	Pro	Met	Cys	Arg	51
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Oy	92	Pro	Ile	Cys	Leu	Pro	Asp	Tyr	---His	Leu	Pro	Pro	110
Db	340	CCCA	CTGTG	ACCAT	TGACT	GTCT	CCAG	ACGAG	CCCAT	CTGCT	CTCT	CTG	399
Oy	111	Arg	Ala	Val	Sala	Gly	Cys	Ser	Pro	Leu	Met	Arg	130
Db	400	CGGG	CGCCG	AGG	CGTGT	GAGCC	CAAT	CAAT	CAAT	CAAT	CAAT	CAAT	459
Oy	131	Met	Ser	Cys	Asp	Arg	Leu	Pro	Val	Leu	Gly	Arg	150
Db	460	CTGG	CGCT	CGAG	AGACT	GCC	CA	GTG	ACG	ACG	AGG	GGC	504
Oy	151	Asn	Arg	Ser	Gln	Ala	Thr	Thr	Ala	Pro	Pro	Arg	170
Db	505	TCT	CCCG	AGG	CCCAT	GTT	ACT	CGG	ACG	AGC	GTG	ATTT	546
Oy	171	Gly	Pro	Pro	Gly	Ala	Pro	Ala	Ser	Gly	Gly	Cys	190
Db	547	-----	ATG	GAT	TTA	GTAA	CGG	AACT	GTAG	AGG	GCA	AGT	594
Oy	191	Lys	Cys	Arg	Gln	Pro	Phe	Val	Pro	Ile	Leu	Syl	206
Db	595	AAAT	GTAG	-----	CTT	ATT	TAG	AGT	CA	CAG	AGC	AT	642
Oy	207	Tyr	Asn	Val	Val	Arg	Thr	Gly	gln	Val	Pro	Asn	223
Db	643	TACA	ACT	AT	GT	AT	CT	CGG	CTA	AA	AGT	TAA	693

RESULT 2
US-09-276-531-45
; Sequence 45, Application US/09276531
; Patent No. 6183968
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga

```

APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Reddy, Roopa
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
NUMBER OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,531
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/079,677
FILING DATE: March 27, 1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lynn E. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0008 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 2039 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: MENTUT03
CLONE: 1256053
US-09-276-531-45
Alignment Scores:
Pred. No.:      Length:      2039
Score:          Matches:     82
Percent Similarity: 49.58%
Best Local Similarity: 34.75%
Query Match:    28.44%
                Mismatches:   84
                Indels:       35
                Gaps:         8
US-09-847-102A-68 (1-235) x US-09-276-531-45 (1-2039)
Qy      4 ProAsProSer-----AlaProProSerLeuLeuLeuLeuLeuAla 18
Db      190 CCCCATCTCGCCGGGATCATGTCTGCCGAGACCCGGGAGGGATCTCTCTCGGGGCC 249
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      19 GluLeuValGlyYrgrAlaIala-----AlaAlaSerIleAlaProval 32
Db      250 GGAGTCTTCGCCTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCAACC 309
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      33 CysGlnGluIleThrValPrometCysatrgilylleglyTYrAsnLeuThrhIsMetPro 52
Db      310 TGTGAGCGCGTCGCGATCCCGCTGTGCAAGTCCCTGACCTGTGAACAATCAATGAATGCC 369
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      53 AsnGlnPheasnhIsasprhrtGlnsrgruIalaglyLeuGluValhIsGlnPheTrPro 72
Db      370 AACCCACTGCACACGACGACACTCAGGCCAACGCCATCTTGGCCATCGAACGTTCCAAAGT 429
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

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COUNTRY: U.S.A.
 ZIP: 94111-4106
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/878,474
 FILING DATE: 18-JUN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/020,150
 FILING DATE: 20-JUN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Siebert, J. Suzanne
 REGISTRATION NUMBER: 28,758
 REFERENCE/DOCKET NUMBER: 3100.002051
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/248-5500
 TELEFAX: 415/362-5418
 INFORMATION FOR SEQ. ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1875 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-878-474-4

Alignment Scores:
 Pred. No.: 1,276-21 Length: 1875
 Score: 360.00 Matches: 83
 Percent Similarity: 52.23% Conservative: 34
 Best Local Similarity: 37.05% Mismatches: 73
 Query Match: 27,488 Indels: 34
 Gaps: 10

US-09-847-102a-68 (1-235) x US-08-878-474-4 (1-1875)

QY 8 A1AProProSerLeuLeuLeuLeuLeuLeuValG1yAArg1Aa1Aa1Aa 27
 DB 366 GCCATACCTGAGCTGGCGCTTCTTATTATCC-----AATGTTACTGTGT 413
 QY 28 SerLyAlAProValCysGlnGlnIleThrValProMetCysArgLyIleGlyTyrAsn 47
 DB 414 TCG-----TGTAGCCTGTGCGGATCCCATGTGCAAACTATGATCGATGGAAC 461
 QY 48 LeuThrHisMetCProAsnGlnPheAsnHisAspThrGlnAspGlnA1aGlyLeuGluVal 67
 DB 462 ATGACCAAGATGCGCCCAACCATCTCCACACAGACATCAAGCCAAATGCTCGCAAT 521
 QY 68 HisGlnPheThrProLeuValGlnIleGlnCysSerProAspLeuArgPhePheLeuCys 87
 DB 522 GAACAGTTTGAAGTTTGCTGACCACTGATGAGCCAGACCTTTGTTCTTGTGTGT 581
 QY 88 ThrMetTyrThrProIleCysLeuProAspTyr---HisLySerLeuProProCysArg 106
 DB 582 GCCATGTATGCCCCCATTTGTACATCATGATTTCCACATGACCAATTAAGCTTCAAG 641
 QY 107 SerValCysGlnArgAlaAlaValGlyCysSerProLeuMetArgGlnTyrGlyPheAla 126
 DB 642 TCCGTGTGCGAAAGGCGCCAGCGGCTGTGAGCCCATTTCTATAAATACCGCACACT 701
 QY 127 TyrProGlnArgMetSerCysAspArgLeuProValLeuGlnLyArgAspAlaGluValLeu 146
 DB 702 TGGCCAGAGAGCTGCGCATGTGAAGAGCTGCCGCTATATGACAGAGA-----GTC 752
 QY 147 CysMetAspTyrAsnArgSerGlnAlaThrThrAlaProProArgArgProPheProAlaLys 166
 DB 753 TGCATCTCC-----CCAGAGGCTATTCGTACACGTGAGACAGAAACAGATTAAAG 803
 QY 167 ProThrLeuProGlyProProGlyAlaProAlaSerGlyGlyGlnCysProAlaGlyGly 186

DB 804 CCAGACTTC-----TCCATGATTCAAACAATGAAATTCGGAAGCGGCAG 851
 QY 187 ProPheValCysLyseCysArgGluProPheValProIle----- 199
 DB 852 GAGCAC---TGTAAATGCAAG-----CCATGAAGGCAACCCAAAGACTAT 896
 QY 200 LeuLyGlnSerHisProLeuTyrAsnLyValArgThrGlyGlnValProAsnCysAla 219
 DB 897 CTCAGAGATTAAT-----TACAATTATGTAATCAGCAAAAGTGAAAGGTGAAA 947
 QY 220 ValProCysTyr 223
 DB 948 GTGAATGCCAC 959

RESULT 5
 US-09-276-531-108
 Sequence 108, Application US/09276531
 Patent No. 6183968
 GENERAL INFORMATION:
 APPLICANT: Bandman, Olga
 APPLICANT: Lal, Preeti
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Yue, Henry
 APPLICANT: Reddy, Roopa
 APPLICANT: Guegler, Karl J.
 APPLICANT: Baughn, Mariah R.
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
 NUMBER OF SEQUENCES: 134
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Word Perfect 6.1 for windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/276,531
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/079,677
 FILING DATE: March 27, 1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Lynn E. Murry, Ph.D.
 REGISTRATION NUMBER: 42,918
 REFERENCE/DOCKET NUMBER: PA-0008 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ. ID NO: 108:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2009 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: BRSTNOT07
 CLONE: 212411
 US-09-276-531-108

Alignment Scores:
 Pred. No.: 4,186-20 Length: 2009
 Score: 342.50 Matches: 74
 Percent Similarity: 50.68% Conservative: 37
 Best Local Similarity: 33.79% Mismatches: 83


```

: TELEPHONE: (650) 855-0555
: TELEFAX: (650) 845-4166
: INFORMATION FOR SEQ ID NO: 23:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 2833 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
: IMMEDIATE SOURCE:
:   LIBRARY: FIBRANT01
:   CLONE: 150629
: US-09-276-531-23

Alignment Scores:
Pred. No.:      8,33e-15      Length:      2833
Score:          282.00      Matches:      65
Percent Similarity: 41.23%      Conservative: 22
Best Local Similarity: 30.81%      Mismatches:  80
Query Match:      21.53%      Indels:      44
DB:                4      Gaps:          6

US-09-847-102A-68 (1-235) x US-09-276-531-23 (1-2833)

QY      33  CysGInGluIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetPro 52
       211 TGTGAACCAATTAAGTCTTCCAGAGTATGAAATGGCCCTCAACAATGAGGTTTTCCT 300
QY      53  AsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrpPro 72
       301 AATCGATGCGGCATTAATGACCAAGATATTGCGCGGTGAATGAGCATTTCTTCCT 360
QY      73  LeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetYTrhPro 92
       361 CTGGCAAACTCTGGAAATGTTCCACCAAACTTGAACCTTCTCGCAAGCATTTGTACCA 420
QY      93  IleCysLeuProAspTyrHisLeysProLeuProProCysArgSerValCysGluArgAla 112
       421 ACCTGCATAGAACAAATTTCAT---GTGGTTCCACCTTGCTGTAACCTTGTGAGAAAGTA 477
QY      113 LysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArgMetSer 132
       478 TATTCGATTCGAAAAAATTAATTGACACTTTGGGATCCGATGGCTGAGAGCTTGA 537
QY      133 CysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMetAspTyrAsnArg 152
       538 TGTGACAGATTCAATTAAGTGTGATGAGACTGTTCCGTGA----- 576
QY      153 SerGluAlaThrThrAlaProProArgProPhe-----ProAlaLysProThrLeuPro 170
       577 -----ACCTTTGATCCACACACAGAAATTTCTTGCTCTCGGAAGAAACA----- 621
QY      171 GlyProProGlyAlaProAlaSerGlyGlyLeuCysProAlaGlyIleGlyProPheValCys 190
       622 -----GAAACAAGTCCAAAGACAGACATTGGATTTGGTGT 654
QY      191 LysCysArgGluProPheValProIleLeuLysGluSerHisProLeuTyrAsnLysVal 210
       655 -----CCAAGCATCTTAAGACT 672
QY      211 ArgThrGlyGln-----ValProAsnCysAlaValAlaProCysTyrGln 224
       673 TCTGGGGGACAGATATTAAGTTTCTGGGAATGACACAGTGTGCGCTCATGCCCAAC 722
QY      225 ProSerPheSerAlaAspGluArgThrPheAla 235
       733 ATGTAATTTAAAGATGATGAGCTAGAGTTTGA 765
DB

```


Db 467 CCTGGCCTGAGATCCTCAATGCGATGATTCTTCT 502

RESULT 13

US-08-937-067-18

Sequence 18, Application US/08937067

Patent No. 643155

GENERAL INFORMATION:

APPLICANT: Melkonian, Samuel

TITLE OF INVENTION: A FAMILY OF GENES ENCODING

TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND

TITLE OF INVENTION: METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MORRISON & FORSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,067

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Lehnardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 1308 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-937-067-18

Alignment Scores:

Pred. No.: 9.91e-12 Length: 1308

Score: 240.50 Matches: 48

Percent Similarity: 49.32% Conservative: 25

Best Local Similarity: 32.43% Mismatches: 51

Query Match: 18.36% Indels: 24

Gaps: 4

US-09-847-102a-68 (1-235) x US-08-937-067-18 (1-1308)

28 SerLyAlaProValCysGlnGluIle-----ThValProMetCysArgGlyIleGly 45

458 ACCAAGCCACCTAGTGGCGGACATCCCGCGGACTGGGGGTGCGCCACACGCGGC 517

46 TyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeu 65

518 TACAAAGATGTGCTGCCCACTGAGACAGACGATGCGGAGTGAAGACAG 577

66 GluValHisGlnIleHetrPrProLeuValGluIleGlnCysSerProAspLeuAlaGlyPhe 85

578 CAGGCCAGACGCTGGGTGCTGCTCAACAGAACTCCAGCCGCGACCGAGTCTTC 637

86 LeuCyMetMetYrThrProIleCysLeuProAspYrHisIlyProLeuProProCys 105

638 CTCTGCTCGCTTTCGCCCGCTGCTGCTG-----GACGGGCCCATCTACCGGTGT 688

106 ArgSerValCysGlnIuArgAlaValAlaGlyCysSerProLeuMetArgIuGlyPhe 125

Db 689 CCTGGCCTGCGAGCCGCGCGACATCGTCCGACCGCGGTATGCACTTCTTGGCTTC 748

126 AlaTyrProGluArgMetSerCysAspArgLeuProValLeuGlyArgAspAlaGluVal 145

749 TACTGACCCGAGATGCTTAAGTGTACACAGTTCC----- 784

146 LeuCyMetAspTyrAsnArgSerGlu-AlaThrThrAlaProPro-----ArgProPh 163

785 -----GAGGGGACGTCTGCATGCGCATGACGCGCCCAAT 820

163 eProAlaIlyProThrLeuPro 170

821 CCCACGAGACCTCCAGCCCC 842

RESULT 14

US-09-276-531-16

Sequence 16, Application US/09276531

Patent No. 6183968

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Lal, Preeti

APPLICANT: Hillman, Jennifer L.

APPLICANT: Yue, Henry

APPLICANT: Reddy, Roopa

APPLICANT: Guegler, Karl J.

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING

TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION

NUMBER OF SEQUENCES: 134

CORRESPONDENCE ADDRESSES:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/276,531

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/079,677

FILING DATE: March 27, 1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Lynn E. Murry, Ph.D.

REGISTRATION NUMBER: 42,918

REFERENCE/DOCKET NUMBER: PA-0008 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 4245 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: BRAITTT21

CLONE: 2526432

US-09-276-531-16

Alignment Scores:

Pred. No.: 4.46e-11 Length: 4245

Score: 240.50 Matches: 48

Percent Similarity: 49.32% Conservative: 25

Best Local Similarity: 32.43% Mismatches: 51

Query Match: 18.368 Indels: 24
 DB: 4 Gaps: 4
 US-09-847-102a-68 (1-235) x US-09-276-531-16 (1-4245)

QY 28 SerLyAlaProValCysGlnGluLeu-----ThrValProMetCysArgGlyIleGly 45
 DB 175 ACCAAGCCACTGACGCTGAGCATGCCCGGAGACTGCGGCTGTCACCAACGCGGC 234
 QY 46 TyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeu 65
 DB 235 TACAGAGATGCTGCTGCCCAACTCTGCGAGCAGACAGAACATGCGGAGGTGAAGCAG 294
 QY 66 GluValHisGlnPheTrpProLeuValGluIleGlnCysSerProAspLeuArgPhePhe 85
 DB 235 CAGCCAGACGCTGGGTGCCCTGCTGCACAAAGAACTGCCAGCGCGGACCCAGGCTTC 354
 QY 86 LeuCysThrMetTyrThrProIleCysLeuProAspTyrHisLeuProLeuProCys 105
 DB 355 CTCTCTGCTCTGCGCGCCGCTGCTGCTG-----GACCGGCCCATCTACCCGCTGT 405
 QY 106 ArgSerValCysGluArgAlaGlyAlaGlyCysSerProLeuMetArgGlnTyrGlyPhe 125
 DB 406 CCGTGGCTCTGCGAGCGCTGCGCACTGCTGCGAGCCGCTCATGCACTTCTGCGCTTC 465
 QY 126 AlaTrpProGluArgMetSerCysAspArgLeuProValLeuGlyArgAspAlaGluVal 145
 DB 466 TACTGGCCCGAGATGCTTAAAGTGTGACAAAGTTCCTCC-----501
 QY 146 LeuCysMetAspTyrAsnArgSerGluAlaThrThrAlaProPro-----ArgProPh 163
 DB 502 -----GAGGGGAGCGTCTGCATGCGCATGACGCGGCCCAT 537
 QY 163 eProAlaLysProThrLeuPro 170
 DB 538 GCCACCAAGCTCCCAAGCCCC 559

RESULT 15
 US-08-893-654B-1
 ; Sequence 1, Application US/08893654B
 ; Patent No. 6165748
 ; GENERAL INFORMATION:
 ; APPLICANT: RACIE, LISA, ET ALIA
 ; TITLE OF INVENTION: Frazzled NUCLEOTIDE SEQUENCES,
 ; TITLE OF INVENTION: EXPRESSION PRODUCTS, COMPOSITIONS AND USES
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENETICS INSTITUTE, INC.
 ; STREET: 87 CAMBRIDGE PARK DRIVE
 ; CITY: CAMBRIDGE
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02140-2387
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/893,654B
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MEINERT, M.C.
 ; REGISTRATION NUMBER: 31,544
 ; REFERENCE/DOCKET NUMBER: GI 5279
 ; TELEPHONE: 617.498.8574
 ; TELEFAX: 617.876.5851
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2190 base pairs
 ; TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 44..889
 US-08-893-654B-1

Alignment Scores:
 Pred. No.: 1,1e-10 Length: 2190
 Score: 231.50 Matches: 52
 Percent Similarity: 50.60% Conservative: 33
 Best Local Similarity: 30.95% Mismatches: 66
 Query Match: 17.67% Indels: 18
 DB: 4 Gaps: 5

US-09-847-102a-68 (1-235) x US-08-893-654B-1 (1-2190)

QY 12 LeuLeuLeuLeuLeuLeuAlaGlnLeuValGlyArgAlaAla-----26
 DB 53 GCTTCTGCTCTCTGCGCTTCCATGCTGCGCGCGCGCGCTTGACATGGATTA 112
 QY 27 ---AlaSerLyAlaProValCysGlnGluLeuThrValProMetCysArgGlyIleGly 45
 DB 113 TCCACCAAGTGGCTTCCATTCCCAAGAGATGGCC-----ATGTCAGATGACCTCGGC 166
 QY 46 TyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeu 65
 DB 167 TACTGGAGATGCGGCTTCCAACTCTTGGGACACACTTAACATGCGCAAGATCCTGCC 226
 QY 66 GluValHisGlnPheTrpProLeuValGluIleGlnCysSerProAspLeuArgPhePhe 85
 DB 227 AAGTCAGACAGATGCGACAGAACTCTTACAGACCGGCTGCCACCTATGCCAGACCTTC 286
 QY 86 LeuCysThrMetTyrThrProIleCysLeuProAspTyrHisLeuProLeuProCys 105
 DB 287 CTATGCTCTCCATTGCGCCCGAGCTGCTGCGACAGCTTC-----ATCAGGCTGTC 337
 QY 106 ArgSerValCysGluArgAlaGlyAlaGlyCysSerProLeuMetArgGlnTyrGlyPhe 125
 DB 338 CCGACAGATGCTGCTGCTTAAGAAACAGTTGCTCTCCAGTTTGGCATGTCATGGCAGC 397
 QY 126 AlaTrpProGluArgMetSerCysAspArgLeuProValLeuGlyArgAspAlaGluVal 145
 DB 398 TCTGCGCTGAGAGCTTGAAGTGTGACAGGTTCCAGCT-----GGGGAAGAC 445
 QY 146 LeuCysMetAspTyrAsnArgSerGluAlaThrThrAlaProProArgProPheProAla 165
 DB 446 ATGTGCTGAGACAC-TCTCAGCAAAAGAGTATCAGTATGCTATTAAGA-----ACTGCC 498
 QY 166 LysProThrLeuProGluProPro 173
 DB 499 AAGCCCAAGCTGCCAGGCGTCCCC 522

Search completed: May 22, 2003, 23:34:37
 Job time : 66 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 22, 2003, 17:58:08 ; Search time 180 Seconds

(without alignments)
1723.937 Million cell updates/sec

Title: US-09-847-102a-68

Perfect score: 1310

Sequence: 1 MARPPSAPSLLLLLLAQL.....PNCAPVQYPSFSADERTFA 235

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2_1/USPTO.spool/US09847102/runat_19052003_160412_844/app.query.fasta_1.391
-DB=published Applications NA -QMT=faefap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=dibc -START=1 -END=-1 -MATRIX=blousum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09847102@cgn2_1.1.57 @runat_19052003_160412_844
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -SPRINTCR=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

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4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	823.5	62.9	2421	9	US-10-152-548-15
3	754	57.6	424	10	US-09-867-701-6119
4	621	47.4	2344	9	US-10-152-548-1

5	440.5	33.6	2259	9	US-10-152-548-13	Sequence 13, Appl
6	398	30.4	4540	10	US-09-917-800A-1684	Sequence 1684, Ap
7	378	28.9	1893	10	US-09-903-170C-10	Sequence 10, Appl
8	378	28.9	1893	10	US-09-903-180B-10	Sequence 10, Appl
9	378	28.9	1893	10	US-09-903-187A-10	Sequence 10, Appl
10	378	28.9	1893	10	US-09-903-171A-10	Sequence 10, Appl
11	378	28.9	1893	10	US-09-903-188A-10	Sequence 10, Appl
12	378	28.9	1893	10	US-09-903-188A-10	Sequence 10, Appl
13	378	28.9	1893	10	US-09-903-125A-10	Sequence 10, Appl
14	372.5	28.4	1484	12	US-10-028-051-3	Sequence 3, Appl
15	372.5	28.4	2039	9	US-09-974-228-15	Sequence 16, Appl
16	372.5	28.4	2039	9	US-10-108-605-118	Sequence 118, App
17	368.5	28.1	1291	9	US-10-028-051-23	Sequence 23, Appl
18	367.5	28.1	1291	12	US-10-028-051-23	Sequence 23, Appl
19	367.5	28.1	2176	10	US-09-903-180B-8	Sequence 8, Appl
20	367	28.0	2176	10	US-09-903-187A-8	Sequence 8, Appl
21	367	28.0	2176	10	US-09-903-171A-8	Sequence 8, Appl
22	367	28.0	2176	10	US-09-903-188A-8	Sequence 8, Appl
23	367	28.0	2176	10	US-09-903-188A-8	Sequence 8, Appl
24	367	28.0	2176	10	US-09-903-125A-8	Sequence 8, Appl
25	367	28.0	2176	10	US-09-903-125A-8	Sequence 8, Appl
26	367	28.0	2176	9	US-10-028-051-1	Sequence 1, Appl
27	366	27.9	2374	12	US-10-028-051-1	Sequence 1, Appl
28	366	27.9	1875	9	US-09-903-170C-4	Sequence 4, Appl
29	366	27.5	1875	10	US-09-903-180B-4	Sequence 4, Appl
30	360	27.5	1875	10	US-09-903-187A-4	Sequence 4, Appl
31	360	27.5	1875	10	US-09-903-171A-4	Sequence 4, Appl
32	360	27.5	1875	10	US-09-903-188A-4	Sequence 4, Appl
33	360	27.5	1875	10	US-09-903-188A-4	Sequence 4, Appl
34	360	27.5	1875	10	US-09-903-125A-4	Sequence 4, Appl
35	360	27.5	1875	10	US-09-903-125A-4	Sequence 4, Appl
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37	308	23.5	2114	10	US-09-780-557-1	Sequence 1, Appl
38	304.5	23.2	2624	9	US-10-152-548-3	Sequence 3, Appl
39	300.5	22.9	484	9	US-09-918-995-23615	Sequence 23615, A
40	299.5	22.9	2828	9	US-10-152-548-7	Sequence 7, Appl
41	284.5	21.7	885	9	US-09-934-483A-2	Sequence 2, Appl
42	284.5	21.7	1799	9	US-09-934-483A-4	Sequence 4, Appl
43	284.5	21.7	1859	9	US-09-934-483A-3	Sequence 3, Appl
44	284.5	21.7	2030	9	US-10-146-474-1	Sequence 1, Appl
45	284	21.7	2523	9	US-10-270-333-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-10-152-548-9
; Sequence 9, Application US/10152548
; Publication No. US20030040051A1
; GENERAL INFORMATION:
; APPLICANT: Bhanot, Punima
; Brink, Marcel
; Harryman, Cindy S.
; Wang, Yanshu
; Heileh, Jen-Chih
; Andrew, Deborah
; Nathans, Jeremy
; Nussle, Roel

TITLE OF INVENTION: Wnt Receptor Compositions and Methods
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Denlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/152,548
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,340
FILING DATE: 11-APR-1997
APPLICATION NUMBER: US 60/015,307
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0167.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2334 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human transmembrane receptor
(frizzled 5) mRNA, Coding region: 321..2078
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-152-548-9
US-09-847-102a-68 (1-235) x US-10-152-548-9 (1-2334)
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Pred. No.: 2,64e-120 Length: 2334
Score: 1310.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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QY 21 ValGlyArgAlaAlaAlaAlaSerLysAlaProValCysGlnGlnLileThrValPromet 40
DB 381 GTGGGCGGGGCGGGCGGGCGGCTGCAAGCGCCCGGTGTGCGAGAAATCAGGCGCCATG 440
QY 41 CysArgGlyTllegLyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
DB 441 TCCCGCGGATCGGCTACCAACCTGACGACATGCCAACCCAGTTCAACACGACGACGAG 500
QY 61 AAspGluAlaGlyLeuGlnLysAlaHisGlnPheThrProLeuValGlnLileGlnCysSerPro 80
DB 501 GACGAGCGGGCGCTGAGGTGACCCAGTCTGGCGCTGTGAGATCCAAATGCTGCGCG 560
QY 81 AAspLeuArgPhePheLeuLeuCysThrMetTyrThrProLleCysLeuProAspTyrHisLys 100
DB 561 GACCTGCGCTTCTCTCTATGCACTATGTAACGCCCATCTGTGCGCCGACATACCAAG 620
QY 101 ProLeuProProCysArgSerValCysGluArgAlaLysAlaGlyCysSerProLeuMet 120
DB 621 CCGCTCCCGCGCGCTGCGGTGAGCGGCGCAAGCGCGGTGCTGCGCGCTGAGT 680
QY 121 ArgGlnTyrGlyPheAlaThrProGluArgMetSerCysAspArgLeuProValLeuGly 140
DB 681 CGGACATAGCGCTTCCCTGCGCGCGGCGGCGATGATGCGACCGCTCCCGGCTGCGGC 740
QY 141 ArgAspAlaGlyValLeuLeuCysMetAspTyrAsnArgSerGlnLileThrAlaProPro 160
DB 741 CGGAGCGCGGAGGTCTCTGTCATGATTAACCGGACGAGGCGCCACCGGCGCGCCCG 800
QY 161 ArgProPheProAlaLysProThrLeuProGlyProProGlyValaProAlaSerGlyGly 180

DB 801 AGGCTTTCCCGCAGCCCAAGCCCTTCAGGCGCGCGAGGGCGCGCGCTCGGGGGGC 860
QY 181 GlnCysProAlaGlyGlyProPheValCysLysCysArgGluProPheValProLleLeu 200
DB 861 GATGCGCGCGCTGGGGCGCGCTGCTGTCGTCAGATGTGCGACCTTCTGTGCTGCTG 920
QY 201 LysGluSerHisProLeuTyrAsnLysValArgThrGlyGlnValProAsnCysAlaVal 220
DB 921 AAGGATCACACCCGCTCTACAAAGGTGGGACGGGCGAGGTGCCCAACTGCCCGGTA 980
QY 221 ProCysTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
DB 981 CCTGCTACACAGCGCTCTTCAGTGCAGCGACGCGCAGCTTCGCC 1025

RESULT 2

US-10-152-548-15
Sequence 15, Application US/10152548
Publication No. US20030040051A1
GENERAL INFORMATION:
APPLICANT: Bhanot, Purnima
Brink, Marcel
Harryman, Cindy S.
Wang, Yanshu
Hsieh, Jen-chih
Andrew, Deborah
Nathans, Jeremy
Nusse, Roel
TITLE OF INVENTION: Wnt Receptor Compositions and Methods
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/152,548
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,340
FILING DATE: 11-APR-1997
APPLICATION NUMBER: US 60/015,307
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0167.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2421 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Mus musculus transmembrane receptor
(frizzled 8) gene, Coding region: 188..2245
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-152-548-15


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Qy 73 LeuValGluIleGlnCysSerProAspLeuArgPheLeuCysThrMetYrThrPro 92
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Db 1276 GGTGTGACCGTA---CTGAGACAGGCGCTGCTCTCTGCGCGCTCTGTGCGAGCGCGCC 1332
Qy 113 LysAlaGlyCysSerProLeuMetArgIntYrGlyPheAlaIleProGluArgMetSer 132
Db 1333 CAG---GGCTGCGAGGACTCATGAACAGTTGCGTTCCAGTGGCCAGACAGCTCAAG 1389
Qy 133 CysAspArgLeuProValIleuGlyArgAspAlaGluValLeuCysMetAspYrAsnArg 152
Db 1390 TCGAGAAAGTCCCTGTGACAGCGC-----GCAGAGAGCTGTGCGTGGCGCAGAACT 1443
Qy 153 SerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuProGlyPro 172
Db 1444 TCCGACAAAGGACCCCGACTCCCTCTGCTGCGGAGTTCTGACACGCAATCCGCGAG 1503
Qy 173 ProGlyAlaProAlaSerGlyGlyGluCysProAlaGly-----Gly 186
Db 1504 CACGGCGGGGTGTGTTACCGCGCGGCTACCGCGAGGTGCGCGCCCGCGAGCGGGA 1563
Qy 187 PropheValCysLysCysArgGluProPheValProIleLeuLysGluSerHisProLeu 206
Db 1564 AAGTTCTCTGCGCG---CGCGCCCTCAGGGTGCCTTCTCACTCAATATCACTTTCTG 1620
Qy 207 TyrAsnLysValArgThrGlyGluValProAsnCysAlaValProCysYrGlnProSer 226
Db 1621 GGGGAGAG-----PheserAlaAspGluArgThrPheAla 235
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RESULT 7
US-09-903-170C-10
; Sequence 10, Application US/09903170C
; Patent No. US20020156249A1
; GENERAL INFORMATION:
; APPLICANT: De Robertis, Edward M.
; APPLICANT: Bouwmeester, Tewis
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
; FILE REFERENCE: 510015-259
; CURRENT APPLICATION NUMBER: US/09/903,170C
; PRIORITY FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/020,150
; PRIORITY FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Human FRZB-1
US-09-903-170C-10

Alignment Scores:
Pred. No.: 2,71e-28 Length: 1893
Score: 378.00 Matches: 84
Percent Similarity: 49.79% Conservative: 34
Best Local Similarity: 35.44% Mismatches: 83
Query Match: 28.85% Indels: 36
DB: 9 Gaps: 8

US-09-847-102a-68 (1-235) x US-09-903-170C-10 (1-1893)
Qy 4 ProAspProSerAla-----ProProSerLeuLeuLeuLeuLeu 17
Db 40 CCGGCCCATCTGCGCGGATCATGTGCTGCGGACGCCGAGAGGAGTCTGCTGCGCGG 99
Qy 18 AlaGlnLeuValGlyArgAlaAla-----AlaAlaSerLysAlaPro 31

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Db 100 GCCGGGCGCTTGGCCCTGCTCTCTGCTCTCCGAGTCCCGGGGCTTGGGCTGCA 159
Qy 32 ValCysGlnGluIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMet 51
Db 160 GCCTGTAGCCCGTCCGATCTCCCTGTGCAAGTCCCTCGGAAACATGACTAAGATG 219
Qy 52 ProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrp 71
Db 220 CCCAACCACTGACACCAAGCACTGAGCCCAAGCCATCTGGCCATGAGACATTCGAA 279
Qy 72 ProLeuValGluIleGlnCysSerProAspLeuArgPheLeuCysThrMetYrThr 91
Db 280 GGTCTGCGGACACCACTGACAGCCGATGCTCTTCTCTCTGCGCAATGACCGC 339
Qy 92 ProIleCysLeuProAspYr---HisLysProLeuProProCysArgSerValCysGlu 110
Db 340 CCCATCTGACCATTTGACTTCCAGACAGACCCATCAAGCCCTGTAAAGTCTGTGCGAG 399
Qy 111 ArgAlaLysAlaGlyCysSerProLeuMetArgIntYrGlyPheAlaIleTrpProGluArg 130
Db 400 CCGGCCCGAGGGGTGTGAGCCCATCTCATCAAGTACCGCCACTCGTGGCGGAGAAC 459
Qy 131 MetSerCysAspArgLeuProValIleuGlyArgAspAlaGluValLeuCysMetAspYr 150
Db 460 CTGGCTCGAGAGAGCTGCACTGATGACAGAGGGG-----GTGTGATC----- 504
Qy 151 AsnArgSerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuPro 170
Db 505 TCTCCCGAGCCATGTTACTGCGAGCGAGCTGATTTTCT----- 546
Qy 171 GlyProGlyAlaProAlaSerGlyGlyGluCysProAlaGlyGlyProPheValCys 190
Db 547 -----ATGGAATCTAGTAAAGAACTGTAGAGGGGCAAGACGTAACGCTGT 594
Qy 191 LysCysArgGluProPheValProIleLeuLysGluSerHisProLeu----- 206
Db 595 AAATGTAG-----CCTATTAGACTACACAGAAAGACTATTTCGGAACAAAT 642
Qy 207 TyrAsnLysValArgThrGlyGluValProAsnCysAlaValProCysYr 223
Db 643 TACAATGATGTCTATTCGGGCTTAAAGTAAAGATTAAGACTTAAGTGCAT 693

RESULT 8
US-09-903-180B-10
; Sequence 10, Application US/09903180B
; Patent No. US20020099171A1
; GENERAL INFORMATION:
; APPLICANT: De Robertis, Edward M.
; APPLICANT: Bouwmeester, Tewis
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
; FILE REFERENCE: 510015-256
; CURRENT APPLICATION NUMBER: US/09/903,180B
; PRIORITY FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/020,150
; PRIORITY FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Human FRZB-1
US-09-903-180B-10

Alignment Scores:
Pred. No.: 2,71e-28 Length: 1893
Score: 378.00 Matches: 84
Percent Similarity: 49.79% Conservative: 34
Best Local Similarity: 35.44% Mismatches: 83
Query Match: 28.85% Indels: 36
DB: 10 Gaps: 8

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; PRIOR APPLICATION NUMBER: US 60/020,150
 ; PRIOR FILING DATE: 1996-06-20
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 1893
 ; TYPE: DNA
 ; ORGANISM: Human FR2B-1
 US-09-903-171A-10

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 2,71e-28	1893	84	34	83	36	8
Percent Similarity: 49.79%						
Best Local Similarity: 35.44%						
Query Match: 28.85%						

US-09-847-102a-68 (1-235) x US-09-903-171A-10 (1-1893)

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QY 4 ProAspProSerAla-----ProProSerLeuLeuLeuLeu 17
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DB 40 CCGGCCCATCTGCGGGATCATGCTCTGCGGAGCCCGGAGGATGCTGCTGCGG 99
   |||||
QY 18 AlaGlnLeuValGlyArgAlaAla-----AlaAlaSerLysAlaPro 31
   |||||
DB 100 GCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 159
   |||||
QY 32 ValCysGlnGlnLeuLeuThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMet 51
   |||||
DB 160 GCGTGGAGCCCGCTGCGCATCCCTGTCGCAAGTCCCTGCGCAACATGACTAAGATG 219
   |||||
QY 52 ProAsnGlnPheAsnHisAspThrGlnAspGlnAlaGlyLeuGlnValHisGlnPheTrp 71
   |||||
DB 220 CCCAACCACTGACACACACACACTGACGCCAAGCCATCTGGCCATCGACGATTCGAA 279
   |||||
QY 72 ProLeuValGlnIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetYrThr 91
   |||||
DB 280 GGTCTGCTGGGACCCACCTGACGACCCGATCTCTCTCTCTCTGTCGATGTAAGCG 339
   |||||
QY 92 ProIleCysLeuProAspTyr---HisLysProLeuProProCysArgSerValCysGln 110
   |||||
DB 340 CCCATCTGACCACTTACCTTCACGACGACGCCCATCAAGCCCTGTAAGTCTGTGCGAG 399
   |||||
QY 111 ArgAlaLysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGlnArg 130
   |||||
DB 400 CCGGCCCGGAGGCGCTGTGAGCCCATATCATCTCAAGTACCGCCACTGTCGCGGAGAAC 459
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QY 131 MetSerCysAspArgLeuProValLeuGlyArgAspAlaGlnValLeuCysMetAspTyr 150
   |||||
DB 460 CTGGCTGCGAGAGAGCTGCGAGTGTACGACAGGCGGCG-----GTGTGATC----- 504
   |||||
QY 151 AsnArgSerGlnAlaThrThrAlaProProArgProPheProAlaLysProThrLeuPro 170
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DB 505 TCTCCCGAGGCCATCTGTAAGTGTGAGCGAGGAGCTGATTTTCT----- 546
   |||||
QY 171 GlyProProGlyValAlaProAlaSerGlyGlyGlnCysProAlaGlyGlyProPheValCys 190
   |||||
DB 547 -----ATGATTTCTAGTAACGAACTGTAGAGGGGCAAGCAGTGAACGCTGT 594
   |||||
QY 191 LysCysArgGlnProPheValProIleLeuLysGlnSerHisProLeu----- 206
   |||||
DB 595 AAATGTAAAG-----CCTATTAGAGTAAACAGAACTATTATTCGGAACAAT 642
   |||||
QY 207 TyrAsnLysValArgThrGlyGlnValProAsnCysAlaValProCysTyr 223
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DB 643 TACAACATAATCTATTCGGGCTAAAGTTAAAGAGATAAAGCTAAGTGCAT 693
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RESULT 11

; Sequence 10, Application US/09903188A
 ; Patent No: US20020128439A1
 ; GENERAL INFORMATION:

; APPLICANT: De Robertis, Edward M.
 ; APPLICANT: Bouwmeester, Tewie
 ; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
 ; TITLE OF INVENTION: Factors
 ; FILE REFERENCE: 510015-258
 ; CURRENT APPLICATION NUMBER: US/09/903,188A
 ; PRIOR FILING DATE: 2001-07-11
 ; PRIOR APPLICATION NUMBER: US 60/020,150
 ; PRIOR FILING DATE: 1996-06-20
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 1893
 ; TYPE: DNA
 ; ORGANISM: Human FR2B-1
 US-09-903-188A-10

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 2,71e-28	1893	84	34	83	36	8
Percent Similarity: 49.79%						
Best Local Similarity: 35.44%						
Query Match: 28.85%						

US-09-847-102a-68 (1-235) x US-09-903-188A-10 (1-1893)

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QY 4 ProAspProSerAla-----ProProSerLeuLeuLeuLeu 17
   |||||
DB 40 CCGGCCCATCTGCGGGATCATGCTCTGCGGAGCCCGGAGGATGCTGCTGCGG 99
   |||||
QY 18 AlaGlnLeuValGlyArgAlaAla-----AlaAlaSerLysAlaPro 31
   |||||
DB 100 GCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 159
   |||||
QY 32 ValCysGlnGlnLeuLeuThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMet 51
   |||||
DB 160 GCGTGGAGCCCGCTGCGCATCCCTGTCGCAAGTCCCTGCGCAACATGACTAAGATG 219
   |||||
QY 52 ProAsnGlnPheAsnHisAspThrGlnAspGlnAlaGlyLeuGlnValHisGlnPheTrp 71
   |||||
DB 220 CCCAACCACTGACACACACACTGACGCCAAGCCATCTGGCCATCGACGATTCGAA 279
   |||||
QY 72 ProLeuValGlnIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetYrThr 91
   |||||
DB 280 GGTCTGCTGGGACCCACCTGACGACCCGATCTCTCTCTCTGTCGATGTAAGCG 339
   |||||
QY 92 ProIleCysLeuProAspTyr---HisLysProLeuProProCysArgSerValCysGln 110
   |||||
DB 340 CCCATCTGACCACTTACCTTCACGACGACGCCCATCAAGCCCTGTAAGTCTGTGCGAG 399
   |||||
QY 111 ArgAlaLysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGlnArg 130
   |||||
DB 400 CCGGCCCGGAGGCGCTGTGAGCCCATATCATCTCAAGTACCGCCACTGTCGCGGAGAAC 459
   |||||
QY 131 MetSerCysAspArgLeuProValLeuGlyArgAspAlaGlnValLeuCysMetAspTyr 150
   |||||
DB 460 CTGGCTGCGAGAGAGCTGCGAGTGTACGACAGGCGGCG-----GTGTGATC----- 504
   |||||
QY 151 AsnArgSerGlnAlaThrThrAlaProProArgProPheProAlaLysProThrLeuPro 170
   |||||
DB 505 TCTCCCGAGGCCATCTGTAAGTGTGAGCGAGGAGCTGATTTTCT----- 546
   |||||
QY 171 GlyProProGlyValAlaProAlaSerGlyGlyGlnCysProAlaGlyGlyProPheValCys 190
   |||||
DB 547 -----ATGATTTCTAGTAACGAACTGTAGAGGGGCAAGCAGTGAACGCTGT 594
   |||||
QY 191 LysCysArgGlnProPheValProIleLeuLysGlnSerHisProLeu----- 206
   |||||
DB 595 AAATGTAAAG-----CCTATTAGAGTAAACAGAACTATTATTCGGAACAAT 642
   |||||
QY 207 TyrAsnLysValArgThrGlyGlnValProAsnCysAlaValProCysTyr 223
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Db 643 TACAACCTATGCTATTCGGGCTAAAGTAAAGATTAAGACTTAAGTCCCAT 693

RESULT 12

US-09-903-323A-10

Sequence 10, Application US/09903323A

Patent No. US20020128440A1

GENERAL INFORMATION:

APPLICANT: De Robertis, Edward M.

APPLICANT: Boumeester, Tewis

TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing

FILE REFERENCE: 510015-261

CURRENT APPLICATION NUMBER: US/09/903,323A

CURRENT FILING DATE: 2001-07-11

PRIOR APPLICATION NUMBER: US 60/020,150

PRIOR FILING DATE: 1996-06-20

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 10

LENGTH: 1893

TYPE: DNA

ORGANISM: Human FRZB-1

US-09-903-323A-10

Alignment Scores:

Pred. No.:	2,71e-28	Length:	1893
Score:	378.00	Matches:	84
Percent Similarity:	49.79%	Conservative:	34
Best Local Similarity:	35.44%	Mismatches:	83
Query Match:	28.85%	Indels:	36
DB:	10	Gaps:	8

US-09-847-102A-68 (1-235) x US-09-903-323A-10 (1-1893)

Qy 4 ProAspProSerAla-----ProProSerLeuLeuLeuLeuLeu 17

Db 40 CTGCCCCATCTGCGCGGATCATGCTGCGCGACCCCGAGGAGATGCTGCTGCGG 99

Qy 18 AlaGlnLeuValGlyArgAlaAla-----AlaAlaSerIysAlaPro 31

Db 100 GCCGGGCTGCTGCGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 159

Qy 32 ValCyGlnGlnIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMet 51

Db 160 GCGCTGTAGCCCGCATCCCGCTGTCAGATCCCGCTGCAAGCATGACTGAATG 219

Qy 52 ProAsnGlnPheAsnHisAspThrGlnAspGlnIleGlyLeuGlnValHisGlnPheTrp 71

Db 220 CCCAACCACTGACACACAGCAGCAGCAGCCCAAGCCATCTGCGCATGACAGATTGCA 279

Qy 72 ProLeuValGlnIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetYrThr 91

Db 280 GGTCTGCTGGGAGCCACCATCTGAGCCCCCATCTGCTCTTCTCTGTCGCGCATGACGG 339

Qy 92 ProIleCysLeuProAspTyr---HisIysProLeuProProCysArgSerValCysGln 110

Db 340 CCCATCTGACACCATTTGACTTCCAGACAGGAGCCCATCAAGCCCTGTAAGCTGTGCGAG 399

Qy 111 ArgAlaIysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGlnArg 130

Db 400 CGGGCCCGGAGGGCTGTGAGCCCATCTGATCATCAAGTACCGCCACTGCGCGCGAGAAC 459

Qy 131 MetSerCysAspArgLeuProValLeuGlnIleGlyArgAspAlaGlnValLeuCysMetAspTyr 150

Db 460 CTGGCTGCGAGAGACTGCGCATGTCATGACAGAGGGC-----GTGTGATC----- 504

Qy 151 AsnArgSerGlnAlaThrThrAlaProArgProPheProAlaLysPheProThrLeuPro 170

Db 505 TCTCCCGAGGCGCATGTTACTGCGAGCGAGCTGATTTTCC----- 546

Qy 171 GlyProProGlnValProAlaSerGlyGlyGlyCysProAlaGlyGlyProPheValCys 190

Db 547 -----ATGATTTCTAGTAACGAACTGTAGAGGGGCAAGCAGTGAACGCTGT 594

Qy 191 LysCysArgGlnProPheValProIleLeuIysGlnSerHisProLeu----- 206

Db 595 AAATGTAG-----CCTATTAGACTACACAGAGAGACTATTTCGGAACAT 642

Qy 207 TyrAsnIysValArgThrGlyGlnValProAsnCysAlaValProCysTyr 223

Db 643 TACAACCTATGCTATTCGGGCTAAAGTAAAGATTAAGACTTAAGTCCCAT 693

RESULT 13

US-09-903-325A-10

Sequence 10, Application US/09903325A

Patent No. US20020128441A1

GENERAL INFORMATION:

APPLICANT: De Robertis, Edward M.

APPLICANT: Boumeester, Tewis

TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing

FILE REFERENCE: 510015-257

CURRENT APPLICATION NUMBER: US/09/903,325A

CURRENT FILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: US 60/020,150

PRIOR FILING DATE: 1996-06-20

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 10

LENGTH: 1893

TYPE: DNA

ORGANISM: Human FRZB-1

US-09-903-325A-10

Alignment Scores:

Pred. No.:	2,71e-28	Length:	1893
Score:	378.00	Matches:	84
Percent Similarity:	49.79%	Conservative:	34
Best Local Similarity:	35.44%	Mismatches:	83
Query Match:	28.85%	Indels:	36
DB:	10	Gaps:	8

US-09-847-102A-68 (1-235) x US-09-903-325A-10 (1-1893)

Qy 4 ProAspProSerAla-----ProProSerLeuLeuLeuLeuLeu 17

Db 40 CTGCCCCATCTGCGCGGATCATGCTGCGCGACCCCGAGGAGATGCTGCTGCGG 99

Qy 18 AlaGlnLeuValGlyArgAlaAla-----AlaAlaSerIysAlaPro 31

Db 100 GCCGGGCTGCTGCGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 159

Qy 32 ValCyGlnGlnIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMet 51

Db 160 GCGCTGTAGCCCGCATCCCGCTGTCAGATCCCGCTGCAAGCATGACTGAATG 219

Qy 52 ProAsnGlnPheAsnHisAspThrGlnAspGlnIleGlyLeuGlnValHisGlnPheTrp 71

Db 220 CCCAACCACTGACACACAGCAGCAGCAGCCCAAGCCATCTGCGCATGACAGATTGCA 279

Qy 72 ProLeuValGlnIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetYrThr 91

Db 280 GGTCTGCTGGGAGCCACCATGTCAGCCCATGCTTCTTCTCTGTCGCGCATGACGG 339

Qy 92 ProIleCysLeuProAspTyr---HisIysProLeuProProCysArgSerValCysGln 110

Db 340 CCCATCTGACACCATTTGACTTCCAGACAGGAGCCCATCAAGCCCTGTAAGCTGTGCGAG 399

Qy 111 ArgAlaIysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGlnArg 130

Db 400 CGGGCCCGGAGGGCTGTGAGCCCATCTGATCATCAAGTACCGCCACTGCGCGAGAAC 459

Qy 131 MetSerCysAspArgLeuProValLeuGlnIleGlyArgAspAlaGlnValLeuCysMetAspTyr 150

Db 460 CTGGCTGCGAGAGACTGCGCATGTCATGACAGAGGGC-----GTGTGATC----- 504

QY 151 AsnArgSerGluAlaThrThrAlaProPheProAlaLysProThrLeuPro 170
::: |||||
Db 505 TCCTCCGAGCCATCGTCTACGCGAGCGAGCTGATTTCT 546
QY 171 GlyProGlyAlaProLaserGlyGlyGlyProAlaGlyGlyProPheValCys 190
547 -----ATGATTCCTAGTAAAGAACTGTAGAGGGGCAAGCAACCGCTGT 594
QY 191 LysCysArgGluProPheValProIleLeuLysGluSerHisProLeu----- 206
595 AAATGTAAG-----CCTATTAGAGCTACACAGAACCTATTTCGGAACAT 642
QY 207 TyrAsnLysValArgThrGlyGlyValProAsnCysAlaValProCysTyr 223
643 TACAACTATGTCATTCGGGCTAAAGTTAAAGATTAAGACTAAGTGCAT 693
Db
RESULT 14
US-10-090-049-3
Sequence 3, Application US/10090049
Publication No. US20030009023A1
GENERAL INFORMATION:
APPLICANT: Luyten, Frank P.
APPLICANT: Moos, Malcolm
APPLICANT: Hoang, Bang
APPLICANT: Wang, Shouwen
TITLE OF INVENTION: ISOLATION AND METHOD OF USING TISSUE
FILE REFERENCE: NIH133.1CPI02
CURRENT APPLICATION NUMBER: US/10/090,049
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 09/289,268
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: PCT/US97/18362
PRIOR FILING DATE: 1997-10-08
PRIOR APPLICATION NUMBER: US 08/822,333
PRIOR FILING DATE: 1997-03-20
PRIOR APPLICATION NUMBER: US 08/729,452
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1484
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-090-049-3
Alignment Scores:
Pred. No.: 7.14e-28 Length: 1484
Score: 372.50 Matches: 82
Percent Similarity: 49.58% Conservative: 35
Best Local Similarity: 34.75% Mismatches: 84
Query Match: 28.44% Indels: 35
Gaps: 8
US-09-847-102a-68 (1-235) x US-10-090-049-3 (1-1484)
QY 4 ProAspProSer-----AlaProPheSerLeuLeuLeuLeuLeuAla 18
190 CCCATCCTCGCGGATCATGCTCGCGGAGCGAGGAGATGCTGCTCGCGGCGC 249
QY 19 GlnLeuValGlyArgAlaAla-----AlaLaserLysAlaProVal 32
250 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 309
QY 33 CysGlnGlnIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetPro 52
310 TGGAGCCCGCTCGCATCCCGCTGTCAGATCCCTCGGAACTGACTAGATGAGCC 369
QY 53 AsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGlnValHisGlnPheTyrPro 72
370 AACCACTGACACACGACACTCAGGCCAACGCCATCTGCCATCGACAGTTGAGAG 429
QY 73 LeuValGlnIleGlnCysSerProAspLeuArgPhePheLeuCysThrMetTyrThrPro 92

Db 430 CGCTGGGACACCCACTGACGAGCCCATCTGCTCTTCTCTGTCATGACCGGCC 489
QY 93 IleCysLeuProAspTyr---HisLysProLeuProProCysArgSerValCysGlnArg 111
490 ATCTTCACCATTTAGTCTACGACGAGCCCATCAAGCCCTGTAGTCTGTGTGCGAGCG 549
QY 112 AlaLysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTyrProGluArgMet 131
550 GCCCGGACGGGTGTGAGCCCATCTACTCATCAAGTACCCGCACTGTCGCGGAGAACTG 609
QY 122 SerCysAspArgLeuProValLeuGlnYargAspAlaGluValLeuCysMetAspTyrXsn 151
610 GCCTCGGAGAGCTCCAGATGACGACAGGGGC-----GTYTGATC-----TCT 654
QY 152 ArgSerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuProGly 171
655 CCCGAGGCCATCTGTTACTGCGGAGCGAGCTGATTTCT----- 693
QY 172 ProProGlyAlaProAlaSerGlyGlyGlyCysProAlaGlyGlyProPheValCysLys 191
694 -----ATGATTCCTAGTAAAGAACTGTAGAGGGGCAAGCAAGTAAAGCTGTAA 744
QY 192 CysArgGluProPheValProIleLeuLysGluSerHisProLeu-----Tyr 207
745 TGTAA-----CCTATTAGAGCTACACAGAACCTATTTCGGAACATTTAC 792
QY 208 AsnLysValArgThrGlyGlyValProAsnCysAlaValProCysTyr 223
793 AACATGTCATTCGGGCTAAAGTTAAAGATTAAGACTAAGTGCAT 840
Db
RESULT 15
US-10-028-051-3
Sequence 3, Application US/10028051
Patent No. US20020147329A1
GENERAL INFORMATION:
APPLICANT: Luyten, Frank P.
APPLICANT: Hoang, Bang
APPLICANT: Moos, Jr., Malcolm
APPLICANT: Wang, Shouwen
TITLE OF INVENTION: ISOLATION AND USE OF TISSUE
FILE REFERENCE: GROWTH INDUCING FR28 PROTEIN
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/028,051
FILING DATE: 19-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/729,452
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bartfield, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: NIH133.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1484 base pairs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_p1us_p2n model

Run on: May 22, 2003, 19:43:08 ; Search time 1516 Seconds
(without alignments)
2510.514 Million cell updates/sec

Title: US-09-847-102a-68
Perfect score: 1310
Sequence: 1 MARPDPSAPSLILLLLAQL.....PNCAPVCYQPSFADERTFA 235

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-O=/cgn2.1/USPTO/US09847102/runat_19052003_160406_736/app_query.fasta_1.391
-DB=EST -QFMT=fastp -SUFFIX=est -MINMATCH=0.1 -DOPEL=0 -DOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=DCT -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09847102.GCGN 1.1.1906 @runat_19052003_160406_736 -NCPU=6 -ICPU=3
-NO MMAP -LARGEBUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
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2: em_esthum:*
3: em_estlin:*
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7: em_estro:*
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9: gb_estc1:*
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12: gb_estc3:*
13: gb_estc4:*
14: gb_estc5:*
15: em_esthum:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
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21: em_gss_vrt:*
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23: em_gss_mam:*
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26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
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4	652	49.8	653	10 BB625724	BB625724 BB625724
5	618.5	47.2	635	10 BB622817	BB622817 BB622817
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7	567	43.3	564	17 AZ475021	AZ475021 IM0292116
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9	524.5	40.0	559	12 BG53236	BG53236 p25d03.y
10	513	39.2	603	9 A1892150	A1892150 mh41e05.y
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12	477	36.4	679	9 A1958244	A1958244 fd02c05.y
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16	419	32.0	937	14 BQ725011	BQ725011 AGENCOURT
17	418	31.9	894	14 BQ736171	BQ736171 AGENCOURT
18	417.5	31.9	658	9 AL651565	AL651565 AL651565
19	414.5	31.6	580	13 B1444839	B1444839 dae79a04.
20	411.5	31.4	1138	14 BM905248	BM905248 AGENCOURT
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22	408	31.1	535	13 BJ107483	BJ107483 BJ107483
23	401.5	30.6	934	14 BQ651465	BQ651465 AGENCOURT
24	399	30.5	595	9 A1794418	A1794418 EC44b09.y
25	398	30.4	494	9 AA017737	AA017737 mh41e05.r
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27	396.5	30.3	918	14 BQ650644	BQ650644 AGENCOURT
28	394.5	30.1	857	14 BQ650917	BQ650917 AGENCOURT
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31	393.5	30.0	572	9 A1437185	A1437185 Eb38g02.y
32	391.5	30.0	2294	11 AK021164	AK021164 Mus muscu
33	391.5	29.9	983	14 BQ645792	BQ645792 AGENCOURT
34	389.5	29.7	1232	14 BQ644208	BQ644208 AGENCOURT
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36	383.5	29.3	1317	14 BQ645492	BQ645492 AGENCOURT
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ALIGNMENTS

RESULT 1
LOCUS BE953717 492 bp mRNA linear EST 29-APR-2002
DEFINITION UI-M-CC1-gzx-c-04-0-UI sl NIH BMP Recl N Mus musculus cDNA clone
ACCESSION BE953717
VERSION BE953717.1 GI:10595515
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriongnathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 492)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene

Best Local Similarity: 97.16% Mismatches: 3
 Query Match: 57.56% Indels: 1
 DB: 9 Gaps: 0

US-09-847-102a-68 (1-235) x AA481448 (1-424)

QY 33 CysGlnGluIleThrValProMetCysArgGlyIleGlyTyrAsnLeuThrHisMetPro 52
 DB 2 TCCAGGAATACACGGTGCCTCATGTGCCCGGCATCGCTACACCTGACGACATGCCCC 61
 QY 53 AangInpheAenHisAspThrGlnAspGlyValIleGlnValHisGlnInpheTrpPro 72
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 DB 122 CTGGTGAGATCCATGCTCTGCGGACCTGCGCTTCTTCTATGCTCTATGACGCCC 181
 QY 93 IleCysLeuProAspTyrHisLysProLeuProProCysArgSerValCysGluArgAla 112
 DB 182 ATCTGTCTGCCGACACCAAGTCGCTGCGCCCTGCGCTGCGTGTGCGAGGC-GCC 240
 QY 113 LysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArgMetSer 132
 DB 241 AAGGCGGCTGCTCGCTGATGCGCCAGTACGGCTTGTCTAGGCGCCAGCGCATGAGC 300
 QY 133 CysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCyseMetAspTyrAsnArg 152
 DB 301 TCCGACCGGCTCCCGGTGTGGGCGCGACCGGAGTCTCTGATGATTAACAACGCC 360
 QY 153 SerGluAlaThrThrAlaProProArgProPheProAlaLysProThrLeuProGlyPro 172
 DB 361 AGCGAGGCCACACGCGCGCCCGCCAGGCTTCCAGCCACGACCCCTTCCAGGCCG 420
 QY 173 Pro 173
 DB 421 CCA 423

RESULT 3
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 DEFINITION Tetradon nigroviridis genome survey sequence TY end of clone 18318 of library G from Tetradon nigroviridis, genomic survey sequence.
 ACCESSION AL221426.1 GI:7880245
 VERSION AL221426
 KEYWORDS GSS: genome survey sequence.
 SOURCE Tetradon nigroviridis
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodoniformes; Tetraodontidae; Tetraodon.
 REFERENCE 1 (bases 1 to 1028)
 ROEST-CROLLIUS, H., JAILLON, O., DASILVA, C., BOUNEAU, L., FISHER, C., BERNOT, A., FIZAMES, C., WINCKER, P., BROTTIER, P., QUETIER, F., SAUTIN, W. and WEISENBACH, J.
 Human gene number estimate provided by genome wide analysis using Tetradon nigroviridis DNA sequence
 TITLE Unpublished
 JOURNAL 2 (bases 1 to 1028)
 REFERENCE ROEST-CROLLIUS, H., JAILLON, O., DASILVA, C., FIZAMES, C., FISHER, C., BOUNEAU, L., BILLAULT, A., QUETIER, F., SAUTIN, W., BERNOT, A. and WEISENBACH, J.
 Characterization and repeat analysis of the compact genome of the freshwater pufferfish tetradon nigroviridis
 TITLE Unpublished
 JOURNAL 3 (bases 1 to 1028)
 REFERENCE Genoscope.
 AUTHORS Direct Submission
 TITLE Submitted (12-APR-2000)
 JOURNAL This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigroviridis

genome. For more information, please take a look at
<http://www.genoscope.cns.fr/tetradon>.
 Location/Qualifiers

FEATURES
 source 1..1028
 /organism="Tetradon nigroviridis"
 /db_xref="taxon:99883"
 /clone="183G18"
 /clone_1b="G"
 /note="Genoscope sequence ID : C0AG183BD09LP1-end : T7"

BASE COUNT 143 a 393 c 301 g 185 t 6 others
 ORIGIN

Alignment Scores:
 Pred. No.: 2,986-44 Length: 1028
 Score: 653.50 Matches: 129
 Percent Similarity: 68.57% Conservative: 15

Best Local Similarity: 61.43% Mismatches: 44
 Query Match: 49.89% Indels: 23
 DB: 17 Gaps: 4

US-09-847-102a-68 (1-235) x CNS02ZUH (1-1028)

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 DB 1 ACGGTGCCCATGTGCMAAGGATCGCTACACCTACCTACATGCCAACCGATTCAAC 60
 QY 57 HisAspThrGlnAspGluAlaGlyLeuGluValHisGlnInpheTrpProLeuValGluIle 76
 DB 61 CACGACACCCAGAGAGAGAGTGGCTGAGATGCACCGATTCTGGCCCTGTGCTATC 120
 QY 77 GlnCysSerProAspLeuArgPhePheLeuCyseThrMetTyrThrProIleCysLeuPro 96
 DB 121 CGCTGCTCCCGGACCTGCTCTTCTTCTCTGACACATGTAACACCCCATCTGCTGCCG 180
 QY 97 AspTyrHisLysProLeuProProCysArgSerValCysGluArgAlaLysAlaCys 116
 DB 181 GACTACCCGACGCGCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 QY 117 SerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArgMetSerCysAspArgLeu 136
 DB 241 TCCCGCTGATGAGCAGTGGCTTCCAGTGGCCCGAGAGATAGCTGCCAGAACTG 300
 QY 137 ProValLeuGlyArgAspAlaGluValLeuCyseMetAspTyrAsnArgSerGluAlaThr 156
 DB 301 CCCGACGTGGGG-----GACGAGGTCTGTGCAATGACGACGAGACGACGAGTCCACC 354
 QY 157 Thr---Ala-ProProArgProPheProAlaLysProThrLeuProGlyProGlyAla 175
 DB 355 ACCCTGGGTCCACCTTCCCAACCCACCCCAAGTCCAGAGCAGACGCGCCGCGCG 414
 QY 175 aProAlaSerGlyGlyGluCysProAlaGlyGlyProPheValCysLysCysArgGluPro 195
 DB 415 GCCCAGTGTGACGGGAG-----TCCCGCTGTGCACTT 449
 QY 195 oPheValProIleLeuLysGluSerHisProLeuTyrAsnLysValAlaGlnr----- 212
 DB 450 CTGTGTGCGCATCCGAGAGGAGGAGTCCCGCCCTACACGACGCGGSGGCGCGCGG 509
 QY 213 -----GlyGlnValProAsnCysAlaValProCysTyrGlnPr 225
 DB 510 CCCCAGCCCGGCGG 569
 QY 225 oSerPheSerLysArgGluArgThrPhe 234
 DB 570 CTCTCTTCAGGAGGAGAACGACCTTC 597

RESULT 4
 Locus BB625724/C 653 bp mRNA linear EST 26-OCT-2001
 DEFINITION BB625724 RIKEN full-length enriched, adult male diencephalon Mus musculus CDNA clone 9350112L18 5', mRNA sequence.
 ACCESSION BB625724
 VERSION BB625724.1 GI:16463940

/note="Organ: placenta; Vector: pT7T3Pac; Site 1: EORI;
Site 2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806."

BASE COUNT 83 a 132 c 174 g 68 t
ORIGIN

Alignment Scores:

Pred. No.: 6, 02e-39 Length: 457
Score: 584.00 Matches: 104
Percent Similarity: 93.81% Conservative: 2
Best Local Similarity: 92.04% Mismatches: 7
Query Match: 44.58% Indels: 0
DB: 10 Gaps: 0

US-09-847-102a-68 (1-235) x AM462410 (1-457)

QY 123 TyrGlyPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuGlyArgAsp 142
DB 455 TACGGCTTGGCTGGCCGACGATGATGGACCGGCTCCGGTGGTGGGCGCGAC 396
QY 143 AlaGluValLeuCysMetSerPyrAsnArgSerGluAlaThrThrAlaProProArgPro 162
DB 395 GCCGAGGTCTCTGCAATGATTACAAACCGACGAGGCCACACCGGCTCCCGCCAGGCC 336
QY 163 PheProAlaIleProThrLeuProGlyProGlyAlaProAlaSerGlyGlyGlyCys 182
DB 335 TTCGGCGTCAAGCCCACTCTCGGCGGCTCGCGGCTCGCGGGAACGACTGC 276
QY 183 ProAlaGlyIleProPheValCysIleCysArgGluProPheValProIleLeuGlyGlu 202
DB 275 GCCGCGGGGGCCCGTGGGTGTGCAAGTGGCGGACCCCTTGGTCCATTGGAAGAG 216
QY 203 SerHisProLeuTyrTrpIleValArgThrGlyValProAsnGlyAlaValProCys 222
DB 215 TCACACCGCTTACCAACAGGTCGACGCGGCGGACGTAACCACTGCGGTCCTGC 156
QY 223 TyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
DB 155 TACCAAGCCTCTTCAAGCCCGACGAGCGACCTTGC 117

RESULT 7

AZ475021 560 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0292116R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0292116 R, DNA sequence.

ACCESSION AZ475021 GI:10633146
VERSION AZ475021.1
KEYWORDS GSS.

SOURCE house mouse.
ORGANISM Mus musculus.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 560)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT
84112, USA

JOURNAL

COMMENT

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Place: 0292 row: 1 column: 16
Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends
High quality sequence stop: 560.
Location/Qualifiers
1..560
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0292116"
/clone_11b="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42mv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[9b]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapored mouse DNA was annealed to
adapored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 106 a 173 c 163 g 118 t
ORIGIN

Alignment Scores:

Pred. No.: 2.01e-37 Length: 560
Score: 567.00 Matches: 101
Percent Similarity: 88.89% Conservative: 11
Best Local Similarity: 80.16% Mismatches: 12
Query Match: 43.28% Indels: 2
DB: 17 Gaps: 1

US-09-847-102a-68 (1-235) x AZ475021 (1-560)

QY 11 SerLeuLeu-----LeuLeuLeuLeuAlaGlnLeuValGlyArgAlaAlaAlaSer 28
DB 181 TCGCTCTATCCGCTTGGCGGTGTCTACAGGCTCTACGGGCTGCCGCGCTTCCGCC 240
QY 29 LysAlaProValCysGlnGluIleThrValProMetCysArgGlyTleGlyTyrAsnLeu 48
DB 241 AAGGAGCTGGCGTCCAGAGATCAGCGGTGCTGTGTCCAAAGGATCGTTACAACTAC 300
QY 49 ThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHis 68
DB 301 ACTTACATGAGCCCAACAGTCAACACGACGACGAGATGAGGCGGCTTGAAGGTGCAC 360
QY 69 GlnPheTrpProLeuValGluIleGlnCysSerProAspLeuArgPhePheLeuCysThr 88
DB 361 CAGTTTGGCGCTGTGTGAATACAGTCTCCCGGACCTCAAGTTCTTTCTGTGAGC 420
QY 89 MetTyrThrProIleCysLeuProAspTyrHisIleCysProLeuProProCysArgSerVal 108
DB 421 ATGTACAGCCCATGTCTGCGAGGATCAAGAAAGCTTGCCTTGTCTGTG 480
QY 109 CysGluArgAlaValAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpPro 128
DB 481 TGTGAACCGCGCAAGCGCGCTCGCGCTCATGCGCCAGTACGAGGTTTGGCT 540
QY 129 GluArgMetSerCysAsp 134
DB 541 GACCCATCGCTGCGAT 558

RESULT 8

BG438433

LOCUS BG438433 564 bp mRNA linear EST 10-MAY-2001
 DEFINITION p825d03.y2 Trichinella spiralis ML CMVspport Jaemer Trichinella
 spiralis cDNA 5' similar to TR:Q13467 Q13467 TRANSMEMBRANE
 RECEPTOR. ; mRNA sequence.
 ACCESSION BG438433
 VERSION BG438433.1 GI:13348081
 KEYWORDS EST.
 SOURCE Trichinella spiralis.
 ORGANISM Eukaryota; Metazoa; Nematoda; Enoplia; Trichocephalida;
 Trichinellidae; Trichinella.
 REFERENCE 1 (bases 1 to 564)
 McCarter,J., Clifton,S., Chiappelli,B., Page,D., Martin,J., Wyle,T.,
 Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
 Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarisvilli,R.,
 Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
 ,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
 Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
 Wilson,R.
 The Washington Univ. Nematode EST Project, 1999
 TITLE The Washington Univ. Nematode EST Project, 1999
 JOURNAL Unpublished (1999)
 COMMENT Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 The library was constructed by Dr. Doug Jaemer
 (djaemer@vetmed.wsu.edu) at Washington State University, Dept. of
 Veterinary Microbiology and Pathology DNA Sequencing by: Washington
 University Genome Sequencing Center St. Louis.
 Seq primer: Sp6
 High quality sequence stop: 417.
 FEATURES
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 Location/Qualifiers
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 /db_xref="taxon:6334"
 /clone_lib="Trichinella spiralis ML CMVspport Jaemer"
 /dev_stage="muscle stage larvae"
 /lab_host="DH10B"
 /note="vector: pCMVspport-7.neo; Site_1: NotI; Site_2: SalI
 ; The library was constructed using mRNA isolated from
 total RNA with oligo-dT cellulose. Total RNA was generated
 from muscle larvae that were isolated from infected rats.
 Larvae were liberated by pepsin/HCl digestion, incubated
 with 1% SDS, treated with RNase and DNase to eliminate
 host nucleic acid contamination, and purified on a Percoll
 gradient. The T. spiralis isolate was obtained from
 Dickson Deepomier (Columbia University). The library was
 provided by Dr. Doug Jaemer (djaemer@vetmed.wsu.edu) and
 colleagues at Washington State University. DNA Sequencing
 by: Washington University Genome Sequencing Center St.
 Louis."
 BASE COUNT 144 a 151 c 149 g 120 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1e-34 Length: 564
 Score: 534.50 Matches: 89
 Percent Similarity: 86.78% Conservative: 16
 Best Local Similarity: 73.55% Mismatches: 15
 Query Match: 40.80% Indels: 1
 DB: 12 Gaps: 1
 US-09-847-102a-68 (1-235) x BG438433 (1-564)
 Oy 33 CysgngluilethvalprowetCyargelyllegllyTyAsnleuThhismetPro 52
 Db 205 TGTGAGAGATCAGCATCCGATGTGCAAGTCGATCGGCTACATATATGCAATGCCC 264
 Oy 53 AenglnPheamHlaAepThrcInaSpqLualaglyLeuGluValHlGlnPheTrPro 72
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 265 AACCAATTCAACACCAACCAAGAGACCCGGCATGAGTGCACCACTTGGCCG 324
 Oy 73 LeuValGluilegInCyserProaspLeuArgPhePheLeuCyethMetTyThrPro 92
 Db 325 CTGGTCGAAATCAACTGTCAGTCCGATTTGGCTTTTCTCTGCAGATGTACACGCCG 384
 Oy 93 IlcYsleuProaspTyThielysProleuProProCyAsargseValCyeglualArgAla 112
 Db 385 ATTGCATAGCGGATATATCCGAACCGTTGCCGGCTGCAGGTGCGTATGCGAACGGGCC 444
 Oy 113 LysAlaGlyCyserProleuMetArgGlnTyGlyPheAlaTPProGluArgMetSer 132
 Db 445 AGGGCCGGCTCGCGCCACTATGCGCGATGCGTTCGAAATGCCCCCAATTGTGAC 504
 Oy 133 CysAspArgLeuProValleuGlyArgAspAlaGluValleuCyMetAspTyArgArg 152
 Db 505 TGCACAGATGTCGGCGTCTTGGTCTGAC---CCGATCATGTTGTGATGATTCGAAACCA 561
 Oy 153 Ser 153
 Db 562 ACT 564
 RESULT 9
 LOCUS BG353236
 DEFINITION p825d03.y1 Trichinella spiralis ML CMVspport Jaemer Trichinella
 spiralis cDNA 5' similar to TR:Q13467 Q13467 TRANSMEMBRANE
 RECEPTOR. ; mRNA sequence.
 ACCESSION BG353236
 VERSION BG353236.1 GI:13181896
 KEYWORDS EST.
 SOURCE Trichinella spiralis.
 ORGANISM Eukaryota; Metazoa; Nematoda; Enoplia; Trichocephalida;
 Trichinellidae; Trichinella.
 REFERENCE 1 (bases 1 to 559)
 McCarter,J., Clifton,S., Chiappelli,B., Page,D., Martin,J., Wyle,T.,
 Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
 Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarisvilli,R.,
 Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
 ,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
 Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
 Wilson,R.
 The Washington Univ. Nematode EST Project, 1999
 TITLE The Washington Univ. Nematode EST Project, 1999
 JOURNAL Unpublished (1999)
 COMMENT Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 The library was constructed by Dr. Doug Jaemer
 (djaemer@vetmed.wsu.edu) at Washington State University, Dept. of
 Veterinary Microbiology and Pathology DNA Sequencing by: Washington
 University Genome Sequencing Center St. Louis.
 Seq primer: Sp6
 High quality sequence stop: 463.
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 Location/Qualifiers
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 /organism="Trichinella spiralis"
 /db_xref="taxon:6334"
 /clone_lib="Trichinella spiralis ML CMVspport Jaemer"
 /dev_stage="muscle stage larvae"
 /lab_host="DH10B"
 /note="vector: pCMVspport-7.neo; Site_1: NotI; Site_2: SalI
 ; The library was constructed using mRNA isolated from
 total RNA with oligo-dT cellulose. Total RNA was generated
 from muscle larvae that were isolated from infected rats.
 Larvae were liberated by pepsin/HCl digestion, incubated
 with 1% SDS, treated with RNase and DNase to eliminate
 host nucleic acid contamination, and purified on a Percoll
 gradient. The T. spiralis isolate was obtained from

[illegible]

```

/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:238315"
/clone_id="NCI_CGAP_Kid11"
/lab host="DH10B"
/notes="Organ: Kidney; Vector: pUT720-Pac (Site 2: Eco RI;
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HNA
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIds 1322376-1323511, 1456007-1456775, and

```

		1500552-1502855). Subtraction by Bento Soares and M Fatima Ronaldo.	
BASE COUNT	89 a	225 c	182 g
ORIGIN			84 t
Alignment Scores:			
Pred. No.:	7.04e-27	Length:	580
Score:	440.00	Matches:	88
Percent Similarity:	59.26%	Conservative:	24
Best local Similarity:	46.56%	Mismatches:	55
Query Match:	33.55%	Indels:	22
DB:	9	Gaps:	5

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US-09-847-102A-68 (1-235) x A1860140 (1-580)
Oy 3 ArGPromAepProSerAlaProProSerLeuLeuLeuLeuLeuAlaGlnLeuValGly 22
Db 12 CGGCAGCGCGCGCGCGCGCCAGTTC-----ACGGGG 44
Oy 23 ArgAlaAlaAlaSerLeuAlaProVal--CysGlnGluLeuThrValPrometCys 42
Db 45 AGAAGGGCATCTCCATCCCGGACACAGGCTTCGTGCAGCGCCATCTCATCCGCTGTGA 104
Oy 42 rglGlyIleGlyTYrZnLeuThrThiMetProAnGlnPheAnhiAspThrGlnAsp 62
Db 105 CGGACATCGCTTACAACACAGACATCATATGCCAAGCTTCGGGCCACACGACGAG 164
Oy 62 IuaIaGlyLeuGluValAlaGlnPheTrpProLeuValGluIleGlyCysSerProAspL 82
Db 165 ACGCAGGCGCTTAgAGGATGCACCGAGTTCATCCGCTGATGAAAGTGACAGTCTGCCCGAAC 224
Oy 82 euArgPhePheLeuCysThiMetTYrThrProIleCysLeuProAspTYrThiAspProL 102
Db 225 TGCGCTTCTTCTGTGCTTCATGACGACCCGTGTGACCGCTG---CTGAACACAGCCA 281
Oy 102 euProProCysArgSerValCysGluArgAlaAlaGlyCysSerProLeuMetArg 122
Db 282 TCCGCGCGTGGCGGCTCTATCTGTGAGCGCGCGCGCAGGAGGTGCGAAGCCCTCATGAAC 341
Oy 122 InTYrGlyPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuGlyArg 142
Db 342 AGTTCGGTTTTCAGGCGCCGACGCCCTGCGCTGTGAGACACTTCCGCGCCACAGGC--- 397
Oy 142 spAlaGluValLeuCysMetAspTYrAsnArgSerGlu-----AlaT 156
Db 398 --GCCGAGCAATCTGCTCGGCGACGAACCACTCCGAGAGCGAGAGTCCCGGCTACTCA 455
Oy 156 hTrhAlaProProArgProPheProAlaLysProThrLeuProGlyProProGlyAlaP 176
Db 456 CCACGCGCGCCCGCGCGGAGCTG-----CAGCCGGAGTGCCGGGAGCACCCCGGAGTGGCC 509
Oy 176 roAlaSerGlyGlyGluCysPro 183
Db 510 CGGGCGGCGGGCGGCTCCCGG 532

```

RESULT	15
LOCUS	BF434722
DEFINITION	BF434722 556 bp mRNA linear EST 29-NOV-2007
ACCESSION	7p03e09.x1 NCI CGAP Ovi18 Homo sapiens cDNA clone IMAGE:3644657 similar to TR:O94816 O94816 FR1ZZUED-7. [1] ;, mRNA sequence.
VERSION	BF434722
KEYWORDS	BF434722.1 GI:11447010
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 556)
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence, stop: 478.

FEATURES

Source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3644657"
/clone_id="NCI CGAP_Ov18"
/tissue_type="fibrosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pT7D-Pac (Pharmacia) with a
modified polylinker; site 1: Not I; site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCATCTGAAGTGGAGCCGCCGGGACATTTTCTTTTCTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library
went through one round of normalisation, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

```

Alignment Scores:

Pred. No.:	7.24e-36	Length:	556
Score:	427.50	Matches:	83
Percent Similarity:	59.14%	Conservative:	27
Best Local Similarity:	44.62%	Mismatches:	51
Query Match:	32.63%	Indels:	25
DB:	12	Gaps:	5

US-09-847-102A-68 (1-235) X BF434722 (1-556)

Qy 12 LeuLeuLeuLeuLeuLeuLaGlnLeuValGlyArgAlaAlaAlaSerValAlaPro 31
 ||| |||:::||||| ||| |||
 Db 8 CTCTGTGCTCTGTGTGGCGCTGTGGGCGCACTGTCCGGGGCGCCGGCGACGG 67
 Qy 32 -----ValCysGlnGluLeuThrVal 38
 ||| |||:::||||| ||| |||
 Db 68 TACCAAGAGAGAAGGAGCATCTCCGTGGCGGACCAAGCGCTTGTCCACCATCTCCATC 127
 Qy 39 ProMetCysArgGlyLeuGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAsp 58
 |||:::||||| ||| |||:::||||| ||| |||
 Db 128 CCGGTGTGCACGAGCACTGCTACCAACAGACCATCTCTCCCAACTCTGTGGGCACACG 187
 Qy 59 ThrGlnAspGluAlaGlyLeuGlnGluValHisGlnPheTrpProLeuValGluLeuGlnCys 78
 |||:::||||| ||| |||:::||||| ||| |||
 Db 188 AACCAAGAGAGAGCGGGGCCCTCGAGGTGCACCAAGTTCTACCGCGTGTGAAGTCAAGT 247
 Qy 79 SerProAspLeuArgPhePheLeuCysThrMetTyrTrpProIleCysLeuProAspTyr 98
 |||:::||||| ||| |||:::||||| ||| |||
 Db 248 TCTCCCAACTCCGCTTTTCTTATCTCTCAAGTATGCGCCGCTGTGCACCGTG---CTC 304
 Qy 99 HisLysProLeuProProCysArgSerValCysGluArgAlaValAlaGlyCysSerPro 118
 :::: |||:::||||| ||| |||:::||||| ||| |||
 Db 305 GATCAGGCGCATCCCGCCGCTGTCTTCTGTGTGCAGCGCGCCCGCAGAGGCTGCAGAGCG 364
 Qy 119 LeuMetArgGlnTyrGlyPheAlaTrpProGluArgMetSerCysAspArgLeuProVal 138
 |||:::||||| ||| |||:::||||| ||| |||
 Db 365 CTCATGAACAAGTTGGGCTTCCAGTGGCGGCGAGCGGCTCGCTGGAGAACCTTCCCGGTG 424
 Qy 139 LeuGlyArgAspAlaGluValLeuCysMetAspTyrAsnArgSerGluAlaThrThrAla 158
 |||:::||||| ||| |||:::||||| ||| |||
 Db 425 CACGGT-----CGGGGCGAGACTCTCGTGGGCGAACAACCTCGAGCGGCTCGGGGGCG 478

[illegible]

Search completed: May 23, 2003, 00:04:42
Job time : 1522 secs

Yu, M.
09/1847102 Page 1
Seq ID 68 w/Inte

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using SW model

Run on: May 19, 2003, 16:34:17 ; Search time 323 Seconds

(without alignments)
469.078 Million cpi1 updates/sec

Title: US-09-847-102a-68

Perfect score: 1310

Sequence: 1 MARPDSPAPSLLLLLLAQL.....PNCAPVCYQPSFSADERTFA 235

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Pending Parents_AA Main:*

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5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/1/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/1/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/1/paa/US089_COMB.pep.*
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19: /cgn2_6/ptodata/1/paa/US095_COMB.pep.*
20: /cgn2_6/ptodata/1/paa/US096_COMB.pep.*
21: /cgn2_6/ptodata/1/paa/US097_COMB.pep.*
22: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*
23: /cgn2_6/ptodata/1/paa/US099_COMB.pep.*
24: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
25: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
26: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1310	100.0	235	US-09-847-102a-68	Sequence 68, Appl
2	1310	100.0	264	US-09-107-112-15	Sequence 15, Appl
3	1310	100.0	585	US-09-107-112-4	Sequence 4, Appl
4	1310	100.0	585	US-09-847-102a-51	Sequence 51, Appl
5	1310	100.0	585	US-10-146-474-9	Sequence 9, Appl
6	1310	100.0	586	US-08-832-340-10	Sequence 10, Appl

7	1310	100.0	586	US-10-152-548-10	Sequence 10, Appl
8	1310	100.0	586	US-60-015-307-10	Sequence 10, Appl
9	1306	99.7	526	US-60-207-360-270	Sequence 270, Appl
10	1306	99.7	542	US-60-229-515-752	Sequence 752, Appl
11	1311	84.8	516	US-09-847-102a-38	Sequence 38, Appl
12	1014	77.4	232	US-60-213-168-237	Sequence 237, Appl
13	1014	77.4	232	US-60-213-170-237	Sequence 237, Appl
14	920	70.2	203	US-60-177-646-3449	Sequence 3449, Ap
15	920	70.2	203	US-60-178-308-2959	Sequence 2959, Ap
16	824	62.9	277	US-09-847-102a-73	Sequence 73, Appl
17	824	62.9	694	PCT-US02-23913-144	Sequence 144, App
18	824	62.9	694	US-09-847-102a-56	Sequence 56, Appl
19	824	62.9	694	US-10-205-823-144	Sequence 144, App
20	824	62.9	694	US-60-228-045-1	Sequence 1, Appl1
21	823.5	62.9	274	US-09-847-102a-74	Sequence 74, Appl
22	823.5	62.9	682	US-08-832-340-16	Sequence 16, Appl
23	823.5	62.9	682	US-10-152-548-16	Sequence 16, Appl
24	823.5	62.9	682	US-60-015-307-16	Sequence 16, Appl
25	823.5	62.9	685	US-09-107-112-10	Sequence 10, Appl
26	823.5	62.9	685	US-09-847-102a-57	Sequence 57, Appl
27	823.5	62.9	685	US-10-146-474-14	Sequence 14, Appl
28	758	57.9	137	US-60-181-425-28	Sequence 28, Appl
29	758	57.9	138	US-60-188-162-4990	Sequence 4990, Ap
30	758	57.9	138	US-60-213-844-265	Sequence 265, App
31	740.5	56.5	599	US-09-847-102a-37	Sequence 37, Appl
32	661	50.5	115	US-09-087-031-11	Sequence 11, Appl
33	661	50.5	115	US-09-087-031-11	Sequence 11, Appl
34	621	47.4	348	US-09-107-112-16	Sequence 16, Appl
35	621	47.4	694	US-08-832-340-2	Sequence 2, Appl1
36	621	47.4	694	US-09-107-112-2	Sequence 2, Appl1
37	621	47.4	694	US-09-614-150-42183	Sequence 42183, A
38	621	47.4	694	US-10-152-548-2	Sequence 2, Appl1
39	621	47.4	694	US-60-015-307-2	Sequence 2, Appl1
40	621	47.4	694	US-60-173-386-1465	Sequence 1465, Ap
41	621	47.4	694	US-60-175-871-1645	Sequence 1645, Ap
42	621	47.4	694	US-60-184-778-1502	Sequence 1502, Ap
43	621	47.4	694	US-60-191-637-41817	Sequence 41817, A
44	621	47.4	694	US-60-191-700-1611	Sequence 1611, Ap
45	619	47.3	115	US-09-087-031E-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-847-102a-68

Sequence 68, Application US/09847102a

GENERAL INFORMATION:

APPLICANT: University of California

APPLICANT: Carson, Dennis A.

APPLICANT: Cort, Maripat

APPLICANT: Rhee, Chae-Seo

APPLICANT: Lorenzo, Leonil M.

TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS

FILE REFERENCE: 22000-20629.00

CURRENT APPLICATION NUMBER: US/09/847,102A

CURRENT FILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 138

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 68

LENGTH: 235

TYPE: PRT

ORGANISM: Homo sapiens

US-09-847-102a-68

Query Match 100.0%; Score 1310; DB 22; Length 235;

Best Local Similarity 100.0%; Pred. No. 75-102;

Matches 235; Conservative 0; Mismatches 0; Indels 0;

QY 1 MARPDSPAPSLLLLLLAQLVGRAAASKAPVCQETIVPCRGIGYNLTMPNPFNDHQ 60

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Db 1 MARPDPASAPSLILLLLLAOLVGRAAAASKAPVCOEITVPMCRGIGYNLTTHMNOFNHDTQ 60
Qy 61 DEAGLEVHQFWPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPLM 120
Db 61 DEAGLEVHQFWPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPLM 120
Qy 121 ROYGFAMBERMSCDRLPYLGRDAEVLCDYNSSEATTAPPRFPFAKPTLPGPAPASGG 180
Db 121 ROYGFAMBERMSCDRLPYLGRDAEVLCDYNSSEATTAPPRFPFAKPTLPGPAPASGG 180
Qy 181 ECPAGGPVCKCRPEFVPIKESHPLYNKVRTGOVNCAPCYOPSFSADERTFA 235
Db 181 ECPAGGPVCKCRPEFVPIKESHPLYNKVRTGOVNCAPCYOPSFSADERTFA 235

```

RESULT 2

```

US-09-107-112-15
Sequence 15, Application US/09107112
GENERAL INFORMATION:

```

```

APPLICANT: Kosik, Kenneth S.
APPLICANT: Morin, Peter
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR TREATING ALZHEIMER'S DISEASE
FILE REFERENCE: 05311/020001
CURRENT APPLICATION NUMBER: US/09/107,112
CURRENT FILING DATE: 1998-06-30
EARLIER APPLICATION NUMBER: US 60/051,359
EARLIER FILING DATE: 1997-06-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 264
TYPE: PRT
ORGANISM: Homo sapiens
US-09-107-112-15

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Query Match 100.0%; Score 1310; DB 15; Length 264;
Best Local Similarity 100.0%; Pred. No. 8e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MARPDPASAPSLILLLLLAOLVGRAAAASKAPVCOEITVPMCRGIGYNLTTHMNOFNHDTQ 60
Db 1 MARPDPASAPSLILLLLLAOLVGRAAAASKAPVCOEITVPMCRGIGYNLTTHMNOFNHDTQ 60
Qy 61 DEAGLEVHQFWPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPLM 120
Db 61 DEAGLEVHQFWPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPLM 120
Qy 121 ROYGFAMBERMSCDRLPYLGRDAEVLCDYNSSEATTAPPRFPFAKPTLPGPAPASGG 180
Db 121 ROYGFAMBERMSCDRLPYLGRDAEVLCDYNSSEATTAPPRFPFAKPTLPGPAPASGG 180
Qy 181 ECPAGGPVCKCRPEFVPIKESHPLYNKVRTGOVNCAPCYOPSFSADERTFA 235
Db 181 ECPAGGPVCKCRPEFVPIKESHPLYNKVRTGOVNCAPCYOPSFSADERTFA 235

```

RESULT 3

```

US-09-107-112-4
Sequence 4, Application US/09107112
GENERAL INFORMATION:

```

```

APPLICANT: Kosik, Kenneth S.
APPLICANT: Morin, Peter
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR TREATING ALZHEIMER'S DISEASE
FILE REFERENCE: 05311/020001
CURRENT APPLICATION NUMBER: US/09/107,112
CURRENT FILING DATE: 1998-06-30
EARLIER APPLICATION NUMBER: US 60/051,359
EARLIER FILING DATE: 1997-06-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 585
TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-107-112-4

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Query Match 100.0%; Score 1310; DB 15; Length 585;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MARPDPASAPSLILLLLLAOLVGRAAAASKAPVCOEITVPMCRGIGYNLTTHMNOFNHDTQ 60
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Qy 61 DEAGLEVHQFWPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPLM 120
Db 61 DEAGLEVHQFWPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPLM 120
Qy 121 ROYGFAMBERMSCDRLPYLGRDAEVLCDYNSSEATTAPPRFPFAKPTLPGPAPASGG 180
Db 121 ROYGFAMBERMSCDRLPYLGRDAEVLCDYNSSEATTAPPRFPFAKPTLPGPAPASGG 180
Qy 181 ECPAGGPVCKCRPEFVPIKESHPLYNKVRTGOVNCAPCYOPSFSADERTFA 235
Db 181 ECPAGGPVCKCRPEFVPIKESHPLYNKVRTGOVNCAPCYOPSFSADERTFA 235

```

RESULT 4

```

US-09-847-102A-51
Sequence 51, Application US/09847102A
GENERAL INFORMATION:

```

```

APPLICANT: University of California
APPLICANT: Carson, Dennis A.
APPLICANT: Corr, Maripat
APPLICANT: Rhee, Chae-Seo
APPLICANT: Lorenzo, Leonil M.
TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
FILE REFERENCE: 22000-20629,00
CURRENT APPLICATION NUMBER: US/09/847,102A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51
LENGTH: 585
TYPE: PRT
ORGANISM: Homo sapiens
US-09-847-102A-51

```

```

Query Match 100.0%; Score 1310; DB 22; Length 585;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MARPDPASAPSLILLLLLAOLVGRAAAASKAPVCOEITVPMCRGIGYNLTTHMNOFNHDTQ 60
Db 1 MARPDPASAPSLILLLLLAOLVGRAAAASKAPVCOEITVPMCRGIGYNLTTHMNOFNHDTQ 60
Qy 61 DEAGLEVHQFWPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPLM 120
Db 61 DEAGLEVHQFWPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPLM 120
Qy 121 ROYGFAMBERMSCDRLPYLGRDAEVLCDYNSSEATTAPPRFPFAKPTLPGPAPASGG 180
Db 121 ROYGFAMBERMSCDRLPYLGRDAEVLCDYNSSEATTAPPRFPFAKPTLPGPAPASGG 180
Qy 181 ECPAGGPVCKCRPEFVPIKESHPLYNKVRTGOVNCAPCYOPSFSADERTFA 235
Db 181 ECPAGGPVCKCRPEFVPIKESHPLYNKVRTGOVNCAPCYOPSFSADERTFA 235

```

RESULT 5

```

US-10-146-47A-9
Sequence 9, Application US/1014647A
GENERAL INFORMATION:

```

```

APPLICANT: Umansky, Samuil

```

Melkonian, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,474
FILING DATE: 14-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-146-474-9
Query Match 100.0%; Score 1310; DB 25; Length 585;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MARDDPSAPSLLLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTTHMPNQHDTQ 60
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DB 61 DEAGLEVHGFVPLVEIQSPDLRFELCTMTYPTICLPYHKPLPCRSVCERAKAGCSPLM 120
QY 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPRRFPFAKPTLPQPPGAPASGG 180
DB 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPRRFPFAKPTLPQPPGAPASGG 180
QY 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPRRFPFAKPTLPQPPGAPASGG 180
DB 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPRRFPFAKPTLPQPPGAPASGG 180
QY 181 ECPAGGFVCKCRPEFVPIIKESHPLYNKVRTGOVNCVAVCYOPSSADERTTA 235
DB 181 ECPAGGFVCKCRPEFVPIIKESHPLYNKVRTGOVNCVAVCYOPSSADERTTA 235
RESULT 6
US-08-832-340-10
Sequence 10 Application US/08832340
GENERAL INFORMATION:
APPLICANT: Bhanot, Purnima
APPLICANT: Brink, Marcel
APPLICANT: Harryman, Cindy S.
APPLICANT: Wang, Yanahu
APPLICANT: Hsieh, Jen-chih
APPLICANT: Andrew, Deborah
APPLICANT: Nathans, Jeremy

APPLICANT: Nussle, Roel
TITLE OF INVENTION: Wnt Receptor Compositions and Methods
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,340
FILING DATE: 11-Apr-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/015,307
FILING DATE: 12-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0167.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 586 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Hf45 protein
US-08-832-340-10
Query Match 100.0%; Score 1310; DB 12; Length 586;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARDDPSAPSLLLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTTHMPNQHDTQ 60
DB 1 MARDDPSAPSLLLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTTHMPNQHDTQ 60
QY 61 DEAGLEVHGFVPLVEIQSPDLRFELCTMTYPTICLPYHKPLPCRSVCERAKAGCSPLM 120
DB 61 DEAGLEVHGFVPLVEIQSPDLRFELCTMTYPTICLPYHKPLPCRSVCERAKAGCSPLM 120
QY 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPRRFPFAKPTLPQPPGAPASGG 180
DB 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPRRFPFAKPTLPQPPGAPASGG 180
QY 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPRRFPFAKPTLPQPPGAPASGG 180
DB 121 ROYGFAMPERMSCDRLPVLGRDAEVLCDYNRSEATTAPRRFPFAKPTLPQPPGAPASGG 180
QY 181 ECPAGGFVCKCRPEFVPIIKESHPLYNKVRTGOVNCVAVCYOPSSADERTTA 235
DB 181 ECPAGGFVCKCRPEFVPIIKESHPLYNKVRTGOVNCVAVCYOPSSADERTTA 235
RESULT 7
US-10-152-548-10
Sequence 10 Application US/10152548
GENERAL INFORMATION:
APPLICANT: Bhanot, Purnima
APPLICANT: Brink, Marcel
APPLICANT: Harryman, Cindy S.
APPLICANT: Wang, Yanahu
APPLICANT: Hsieh, Jen-chih
APPLICANT: Andrew, Deborah

Nathans, Jeremy
Nusse, Roel
TITLE OF INVENTION: Wnt Receptor Compositions and Methods
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/152,548
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,340
FILING DATE: 11-APR-1997
APPLICATION NUMBER: US 60/015,307
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0167,30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0980
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 586 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Hfz5 protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-152-548-10
Query Match 100.0%; Score 1310; DB 25; Length 586;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARPPSAAPSLILLALLAQLVGRRAAASKAPVCOEITVPMCRGIGYNTLTHMPNDFHDTQ 60
DB 1 MARPPSAAPSLILLALLAQLVGRRAAASKAPVCOEITVPMCRGIGYNTLTHMPNDFHDTQ 60
QY 61 DEAGLEVHGFVPLVEIQCSPLRFLCTMYTPICLPDYHKPLPPCRSCVCEKAKGCSPLM 120
DB 61 DEAGLEVHGFVPLVEIQCSPLRFLCTMYTPICLPDYHKPLPPCRSCVCEKAKGCSPLM 120
QY 121 ROYGFAMPERMSCDRPLVGRDAEVLCDVYRSEATTAPRPFPAPKPTLPGPAPASGG 180
DB 121 ROYGFAMPERMSCDRPLVGRDAEVLCDVYRSEATTAPRPFPAPKPTLPGPAPASGG 180
QY 181 ECPAGGPFVCKCRPFVPLIKESHPLYNKRTGQVPCAVPCYSPSADERTFA 235
DB 181 ECPAGGPFVCKCRPFVPLIKESHPLYNKRTGQVPCAVPCYSPSADERTFA 235

RESULT 8
US-60-015-307-10
Sequence 10, Application US/60015307
GENERAL INFORMATION:
APPLICANT: Bhanot, Purnima
APPLICANT: Brink, Marcel

APPLICANT: Hairyman, Cindy S.
APPLICANT: Wang, Yanshu
APPLICANT: Hsieh, Jen-chih
APPLICANT: Andrew, Deborah
APPLICANT: Nathans, Jeremy
APPLICANT: Nusse, Roel
TITLE OF INVENTION: Wnt Receptor Compositions and Methods
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/015,307
FILING DATE: 11-APR-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0980
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 586 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Hfz5 protein
US-60-015-307-10
Query Match 100.0%; Score 1310; DB 27; Length 586;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARPPSAAPSLILLALLAQLVGRRAAASKAPVCOEITVPMCRGIGYNTLTHMPNDFHDTQ 60
DB 1 MARPPSAAPSLILLALLAQLVGRRAAASKAPVCOEITVPMCRGIGYNTLTHMPNDFHDTQ 60
QY 61 DEAGLEVHGFVPLVEIQCSPLRFLCTMYTPICLPDYHKPLPPCRSCVCEKAKGCSPLM 120
DB 61 DEAGLEVHGFVPLVEIQCSPLRFLCTMYTPICLPDYHKPLPPCRSCVCEKAKGCSPLM 120
QY 121 ROYGFAMPERMSCDRPLVGRDAEVLCDVYRSEATTAPRPFPAPKPTLPGPAPASGG 180
DB 121 ROYGFAMPERMSCDRPLVGRDAEVLCDVYRSEATTAPRPFPAPKPTLPGPAPASGG 180
QY 181 ECPAGGPFVCKCRPFVPLIKESHPLYNKRTGQVPCAVPCYSPSADERTFA 235
DB 181 ECPAGGPFVCKCRPFVPLIKESHPLYNKRTGQVPCAVPCYSPSADERTFA 235

RESULT 9
US-60-207-360-270
Sequence 270, Application US/60207360
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000591

CURRENT APPLICATION NUMBER: US/60/207,360
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 386
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 270
LENGTH: 526
TYPE: PRF
ORGANISM: HUMAN
US-60-207-360-270

Query Match 99.7%; Score 1306; DB 27; Length 526;
Best Local Similarity 99.6%; Pred. No. 3.9e-101;
Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARDPSPAPSLILLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTTHMPNQHDTQ 60
DB 1 MARDPSPAPSLILLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTTHMPNQHDTQ 60
QY 61 DEAGLEVHGFVPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPCRSVCERAKAGCSPLM 120
DB 61 DEAGLEVHGFVPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPCRSVCERAKAGCSPLM 120
QY 121 ROYGFAMPERMSCDRLPVLGDAEVLCDYNRSEATTAPEPPPAKPTLPGPAPASGG 180
DB 121 ROYGFAMPERMSCDRLPVLGDAEVLCDYNRSEATTAPEPPPAKPTLPGPAPASGG 180
QY 181 ECPAGGFVCKCRBPFPVILKESHPLYNKVRTGOVPCAVCYOFSFADERTFA 235
DB 181 ECPAGGFVCKCRBPFPVILKESHPLYNKVRTGOVPCAVCYOFSFADERTFA 235

RESULT 10
US-60-229-515-752
Sequence 752, Application US/60229515
GENERAL INFORMATION:

APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
FILE REFERENCE: CL0000776
CURRENT APPLICATION NUMBER: US/60/229,515
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 2013
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 752
LENGTH: 542
TYPE: PRF
ORGANISM: HUMAN
US-60-229-515-752

Query Match 99.7%; Score 1306; DB 27; Length 542;
Best Local Similarity 99.6%; Pred. No. 4e-101;
Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARDPSPAPSLILLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTTHMPNQHDTQ 60
DB 1 MARDPSPAPSLILLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTTHMPNQHDTQ 60
QY 61 DEAGLEVHGFVPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPCRSVCERAKAGCSPLM 120
DB 61 DEAGLEVHGFVPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPCRSVCERAKAGCSPLM 120
QY 121 ROYGFAMPERMSCDRLPVLGDAEVLCDYNRSEATTAPEPPPAKPTLPGPAPASGG 180
DB 121 ROYGFAMPERMSCDRLPVLGDAEVLCDYNRSEATTAPEPPPAKPTLPGPAPASGG 180
QY 181 ECPAGGFVCKCRBPFPVILKESHPLYNKVRTGOVPCAVCYOFSFADERTFA 235
DB 181 ECPAGGFVCKCRBPFPVILKESHPLYNKVRTGOVPCAVCYOFSFADERTFA 235

RESULT 11
US-09-847-102a-38

Sequence 38, Application US/09847102A
GENERAL INFORMATION:
APPLICANT: University of California
APPLICANT: Carson, Dennis A.
APPLICANT: Corr, Maripat
APPLICANT: Rhee, Chae-Seo
APPLICANT: Malini, Sen
APPLICANT: Lorenzo, Leonil M.
TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
FILE REFERENCE: 22000-20629.00
CURRENT APPLICATION NUMBER: US/09/847,102A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 516
TYPE: PRF
ORGANISM: Homo sapiens
US-09-847-102a-38

Query Match 84.8%; Score 1111; DB 22; Length 516;
Best Local Similarity 87.2%; Pred. No. 1e-84; 0; Indels 30; Gaps 1;
Matches 205; Conservative 0; Mismatches 0;

QY 1 MARDPSPAPSLILLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTTHMPNQHDTQ 60
DB 1 MARDPSPAPSLILLLLAQLVGRRAAASKAPVCOEITVPMCRGIGYNLTTHMPNQHDTQ 60
QY 61 DEAGLEVHGFVPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPCRSVCERAKAGCSPLM 120
DB 61 DEAGLEVHGFVPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPCRSVCERAKAGCSPLM 120
QY 121 ROYGFAMPERMSCDRLPVLGDAEVLCDYNRSEATTAPEPPPAKPTLPGPAPASGG 180
DB 121 ROYGFAMPERMSCDRLPVLGDAEVLCDYNRSEATTAPEPPPAKPTLPGPAPASGG 180
QY 181 ECPAGGFVCKCRBPFPVILKESHPLYNKVRTGOVPCAVCYOFSFADERTFA 235
DB 181 ECPAGGFVCKCRBPFPVILKESHPLYNKVRTGOVPCAVCYOFSFADERTFA 205

RESULT 12
US-60-213-169-237
Sequence 237, Application US/60213169
GENERAL INFORMATION:

APPLICANT: BEASLEY, ELLEN
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
FILE REFERENCE: CL0000699
CURRENT APPLICATION NUMBER: US/60/213,169
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 678
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 237
LENGTH: 232
TYPE: PRF
ORGANISM: HUMAN
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1) ... (232)
OTHER INFORMATION: Xaa = Any Amino Acid
US-60-213-169-237

Query Match 77.4%; Score 1014; DB 27; Length 232;
Best Local Similarity 98.3%; Pred. No. 6.2e-77;
Matches 178; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 55 FNHDTQDEAGLEVHGFVPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPCRSVCERAKA 114
DB 1 FNHDTQDEAGLEVHGFVPLVEIQSPDLRFLLCTMYTPICLPDYHKPLPCRSVCERAKA 60

Oy	115	GCSPLMRQYGFAMPEPRMSCDRLPVLGRAEVLAMDYNRSSEATTAPRPFPFAKPTLPSPG	174
Db	61	GCSPLVRQYGFAMPEPRMSCDRLPVLGRDAEVLAMDYNRSEATTAPRPFPFAKPTLPSPG	120
Oy	175	APASGCPCPAGCPFYCKCRBEPVPIIKESHPLNNKVRTGOVPNCANVCYOBSFSADERTF	234
Db	121	APASGCPCPAGGPFYCKCRBEPVPIIKESHPLNNKVRTGOVPNCAVPCYOBSFSADERTF	180
Oy	235	A 235	
Db	181	A 181	

```

RESULT 13
US-60-213-170-237
: Sequence 237, Application US/60213170
: GENERAL INFORMATION:
: APPLICANT: BEASLEY, ELLEN
: TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
: TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
: TITLE OF INVENTION: PROTEINS, AND USRS THEREOF
: FILE REFERENCE: C1000699
: CURRENT APPLICATION NUMBER: US/60/213,170
: CURRENT FILING DATE: 2000-06-22
: NUMBER OF SEQ ID NOS: 678
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 237
: LENGTH: 232
: TYPE: PRT
: ORGANISM: HUMAN
: FEATURE:
: NAME/KEY: VARIANT
: LOCATION: (1)...(232)
: OTHER INFORMATION: Xaa = Any Amino Acid
US-60-213-170-237

```

Query Match	77.4%	Score 1014	DB 27	Length 232
Best Local Similarity	98.3%	Pred. No. 6	2e-77	
Matches 178	Conservative 2	Mismatches 1	Indels 0	Gaps 0
QY	55	FHHDTODEAGLEVHOFWPLVEIQCSFDLRFPLCTMYTPTCLPDYHKLPDPCRSVCERAKA	114	
Db	1	FHHDTODEAGLEVHOGWPLVEIQCSFDLRFPLCSMYTPTCLPDYHKLPDPCRSVCERAKA	60	
QY	115	GCSPILROYGFAFMPBMSGCDRLPYLGRDAEVLICMDYNRESEATTAPRRPPAKPTLGPBG	174	
Db	61	GCSPILROYGFAFMPBMSGCDRLPYLGRDAEVLICMDYNRESEATTAPRRPPAKPTLGPBG	120	
QY	175	APASGGECPAGAPFVCKCEPFVPLIKESHPLYNKRTQGVNCAVPCYQPSFSADERTF	234	
Db	121	APASGGECPAGAPFVCKCEPFVPLIKESHPLYNKRTQGVNCAVPCYQPSFSADERTF	180	
QY	235	A 235		
Db	181	A 181		

```

RESULT 14
US-60-177-646-3449
; Sequence 3449, Application US/60177646
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS
; FILE REFERENCE: CLO00210
; CURRENT APPLICATION NUMBER: US/60/177, 646
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 4226
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3449
; LENGTH: 203
; TYPE: PRT

```

[illegible]

```

RESULT 15
US-60-178-308-2959
: Sequence 2959, Application US/60178308
: GENERAL INFORMATION:
: APPLICANT: Bonazzi, Vivien
: TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
: TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
: TITLE OF INVENTION: PROTEINS, AND USES THEREOF
: FILE REFERENCE: CL000204
: CURRENT APPLICATION NUMBER: US/60/178,308
: CURRENT FILING DATE: 2000-01-27
: NUMBER OF SEQ ID NOS: 344
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2959
: LENGTH: 203
: TYPE: PRT
: ORGANISM: HUMAN
US-60-178-308-2959

```

	Query Match	70.2%: Score 920	DB 270	Length 203
Best Local Similarity	99.4%	Pred. No. 4.5e-69		
Matches 162	Conservative 1	Mismatches 0	Indels 0	Gaps 0
QY	73	LVEIOCSDDLRFELCTMYTPTICLPDYHKPLPRCSRVCERAKAGCSPLMRQYGFAMPERMS	132	
DB	1	LVEIGCSDDLRFELCSMTPTICLPDYHKPLPRCSRVCERAKAGCSPLMRQYGFAMPERMS	60	
QY	133	CDRLVLVGRDAEVLCDMDYNRSFATTAAPRPFPKATLTGPRGAPASGEGCPAGGFVYCKC	192	
DB	61	CDRLVLVGRDAEVLCDMDYNRSFATTAAPRPFPKATLTGPRAPASGEGCPAGGFVYCKC	120	
QY	193	REPFPVILKESHPLINKYRTGQVPCAVCPQSPSADERTPA	235	
DB	121	REPFPVILKESHPLINKYRTGQVPCAVCPQSPSADERTPA	163	

Search completed: May 19, 2003, 16:41:30
Job time : 326 secs

GenCore version 5.1.4.ps.4578
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OM protein - protein search, using SW model

Run on: May 19, 2003, 16:34:42 ; Search time 90 Seconds
(without alignment)
455.046 Million cell updates/sec

Title: US-09-847-102a-68
Perfect score: 1310
Sequence: 1 MARPPDPAPSLLLLLLAQL.....PNCAPCYQPSFADERTFA 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 797317 seqs, 174272795 residues

Total number of hits satisfying chosen parameters: 797317

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA New:
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	1310	100.0	585	US-10-301-764-9	Sequence 9, Appl
2	1310	100.0	585	US-10-285-976-47	Sequence 47, Appl
3	1300	99.2	233	US-10-264-825-35	Sequence 35, Appl
4	824	62.9	694	US-10-311-623-6	Sequence 6, Appl
5	824	62.9	694	US-10-285-976-53	Sequence 53, Appl
6	824	62.9	694	US-10-115-678-250	Sequence 250, App
7	824	62.9	694	US-10-112-944-250	Sequence 250, App
8	824	62.9	694	US-60-452-680-21108	Sequence 21108, A
9	823.5	62.9	685	US-10-301-764-14	Sequence 14, Appl
10	818	62.4	275	US-10-264-825-38	Sequence 38, Appl
11	477	36.4	565	US-10-301-764-8	Sequence 8, Appl
12	477	36.4	565	US-10-225-567A-382	Sequence 382, App
13	477	36.4	565	US-10-285-976-41	Sequence 41, Appl
14	472.5	36.1	563	US-60-453-135-9598	Sequence 9598, Ap
15	472.5	36.1	563	US-60-453-050-9598	Sequence 9598, Ap
16	469	35.8	242	US-10-264-825-32	Sequence 32, Appl
17	461	35.2	574	US-10-285-976-51	Sequence 51, Appl
18	448	34.2	251	US-10-264-825-37	Sequence 37, Appl
19	440.5	33.6	572	US-10-301-764-13	Sequence 13, Appl
20	415	31.7	647	US-10-285-976-39	Sequence 39, Appl
21	412.5	31.5	318	US-10-264-825-31	Sequence 31, Appl
22	394.5	30.1	591	US-10-285-976-55	Sequence 55, Appl
23	393	30.0	229	US-10-264-825-39	Sequence 39, Appl
24	388	29.6	597	US-10-017-161-800	Sequence 800, App
25	384	29.3	225	US-10-264-825-40	Sequence 40, Appl
26	384	29.3	581	US-10-285-976-57	Sequence 57, Appl

27	372.5	28.4	371	US-09-949-016-7544	Sequence 7544, Ap
28	372	28.4	325	US-60-453-135-11861	Sequence 11861, A
29	372	28.4	325	US-60-453-135-11862	Sequence 11862, A
30	372	28.4	325	US-60-453-050-11861	Sequence 11861, A
31	372	28.4	325	US-60-453-050-11862	Sequence 11862, A
32	366.5	28.0	605	US-10-359-493-6297	Sequence 6297, Ap
33	366	27.9	325	US-09-610-6508-5	Sequence 5, Appl
34	345.5	26.4	368	US-09-724-676-55475	Sequence 55475, A
35	345.5	26.4	368	US-09-724-676A-55475	Sequence 55475, A
36	342.5	26.1	347	US-09-610-6508-2	Sequence 2, Appl
37	342.5	26.1	368	US-09-610-6508-4	Sequence 4, Appl
38	342.5	26.1	368	US-10-405-027-3728	Sequence 3728, Ap
39	342.5	26.1	368	US-60-452-680-12637	Sequence 12637, A
40	339.5	25.9	568	US-10-359-493-5205	Sequence 5205, Ap
41	338.5	25.8	346	PCT-US02-34777-329	Sequence 329, App
42	338.5	25.8	346	PCT-US02-37431-189	Sequence 189, App
43	338.5	25.8	346	US-10-283-017-329	Sequence 329, App
44	338.5	25.8	346	US-10-301-822-189	Sequence 189, App
45	338.5	25.8	346	US-10-126-052A-423	Sequence 423, App

ALIGNMENTS

RESULT 1
US-10-301-764-9
Sequence 9, Application US/10301764
GENERAL INFORMATION:
APPLICANT: Umansky, Samuil
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,764
FILING DATE: 20-Nov-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-301-764-9
Query Match 100.0%; Score 1310; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 1,5e-90;
Matches 235; Conservative 0; Mismatches 0; Indels 0;

```

Qy 1 MARPPSAPSLILLILLLAQLVGRAAAASKAPVCOEITVPMCRGIGYNLTMPNPFNHDQ 60
Db 1 MARPPSAPSLILLILLLAQLVGRAAAASKAPVCOEITVPMCRGIGYNLTMPNPFNHDQ 60
Qy 61 DEAGLEVHOFWFLVEIQCSPLRFFLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPILM 120
Db 61 DEAGLEVHOFWFLVEIQCSPLRFFLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPILM 120
Qy 121 ROYGFAMPERMSCDRLPYLGRDAEVLICMDYNSSEATTAPRPFPAKPTLPGPFGAPASGG 180
Db 121 ROYGFAMPERMSCDRLPYLGRDAEVLICMDYNSSEATTAPRPFPAKPTLPGPFGAPASGG 180
Qy 181 ECPAGGPFVCKCRPEFPVILKESHPLYNKVRTGOVPCNCAVPCYOPSFSADERTFA 235
Db 181 ECPAGGPFVCKCRPEFPVILKESHPLYNKVRTGOVPCNCAVPCYOPSFSADERTFA 235

```

```

RESULT 2
US-10-285-976-47
; Sequence 47, Application US/10285976
; GENERAL INFORMATION:

```

```

; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Malini, Sen
; APPLICANT: Wu, Christina
; APPLICANT: Leonil, Lorenzo M.
; APPLICANT: Corr, Maripat
; APPLICANT: Carson, Dennis A.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
; FILE REFERENCE: 023070-130320US
; CURRENT APPLICATION NUMBER: US/10/285,976
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/287,995
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: WO PCT/US02/13802
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human frizzleds (Fzds)
US-10-285-976-47

```

```

Query Match 100.0%; Score 1310; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.5e-90;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MARPPSAPSLILLILLLAQLVGRAAAASKAPVCOEITVPMCRGIGYNLTMPNPFNHDQ 60
Db 1 MARPPSAPSLILLILLLAQLVGRAAAASKAPVCOEITVPMCRGIGYNLTMPNPFNHDQ 60
Qy 61 DEAGLEVHOFWFLVEIQCSPLRFFLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPILM 120
Db 61 DEAGLEVHOFWFLVEIQCSPLRFFLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPILM 120
Qy 121 ROYGFAMPERMSCDRLPYLGRDAEVLICMDYNSSEATTAPRPFPAKPTLPGPFGAPASGG 180
Db 121 ROYGFAMPERMSCDRLPYLGRDAEVLICMDYNSSEATTAPRPFPAKPTLPGPFGAPASGG 180
Qy 181 ECPAGGPFVCKCRPEFPVILKESHPLYNKVRTGOVPCNCAVPCYOPSFSADERTFA 235
Db 181 ECPAGGPFVCKCRPEFPVILKESHPLYNKVRTGOVPCNCAVPCYOPSFSADERTFA 235

```

```

RESULT 3
US-10-264-825-35
; Sequence 35, Application US/10264825
; GENERAL INFORMATION:

```

```

; APPLICANT: He, Biao
; APPLICANT: You, Liang
; APPLICANT: Xu, Zhidong
; APPLICANT: Jablons, David M.
; TITLE OF INVENTION: Methods for Treating Cancer by
; TITLE OF INVENTION: Inhibiting Wnt Signalling
; FILE REFERENCE: 023070-125600US
; CURRENT APPLICATION NUMBER: US/10/264,825
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(233)
; OTHER INFORMATION: human frizzled-5 peptide sequence
US-10-264-825-35

```

```

Query Match 99.2%; Score 1300; DB 6; Length 233;
Best Local Similarity 100.0%; Pred. No. 3.8e-90;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MARPPSAPSLILLILLLAQLVGRAAAASKAPVCOEITVPMCRGIGYNLTMPNPFNHDQ 60
Db 1 MARPPSAPSLILLILLLAQLVGRAAAASKAPVCOEITVPMCRGIGYNLTMPNPFNHDQ 60
Qy 61 DEAGLEVHOFWFLVEIQCSPLRFFLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPILM 120
Db 61 DEAGLEVHOFWFLVEIQCSPLRFFLCTMYTPICLPDYHKPLPPCRSVCERAKAGCSPILM 120
Qy 121 ROYGFAMPERMSCDRLPYLGRDAEVLICMDYNSSEATTAPRPFPAKPTLPGPFGAPASGG 180
Db 121 ROYGFAMPERMSCDRLPYLGRDAEVLICMDYNSSEATTAPRPFPAKPTLPGPFGAPASGG 180
Qy 181 ECPAGGPFVCKCRPEFPVILKESHPLYNKVRTGOVPCNCAVPCYOPSFSADERT 233
Db 181 ECPAGGPFVCKCRPEFPVILKESHPLYNKVRTGOVPCNCAVPCYOPSFSADERT 233

```

```

RESULT 4
US-10-311-623-6
; Sequence 6, Application US/10311623
; GENERAL INFORMATION:

```

```

; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.
; APPLICANT: KALLICK, Deborah A.; TRIBOULET, Catherine M.
; APPLICANT: YUE, Henry; NGUYEN, Daniel B.
; APPLICANT: TANG, Y. Tom; LAL, Preeti G.
; APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Yalda
; APPLICANT: LU, Dyrng Alma M.; GRAUL, Richard C.
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: HARALJA, April J. A.; BAUGHN, Mariah R.
; APPLICANT: BANDMAN, Olga; ARVIZU, Chandra S.
; APPLICANT: YANG, Junming; XU, Yuming
; APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.
; APPLICANT: DING, Li; SANTANWALA, Madhusudan M.
; APPLICANT: DUGGAN, Brendan M.; LU, Yan
; TITLE OF INVENTION: RECEPTORS
; FILE REFERENCE: PR-0793 USN
; CURRENT APPLICATION NUMBER: US/10/311,623
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 01/19942
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/214,027
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/228,045
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/255,104
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program

```

```
SEQ ID NO 6
LENGTH: 694
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 1534444CD1
US-10-311-623-6
```

```
Query Match          62.9%; Score 824; DB 6; Length 694;
Best Local Similarity 59.9%; Pred. No. 5.2e-54;
Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;
```

```
QY 11 SLL--LTLIAQLVGRAAAAKAPVCOEITVPMCRGIGYNTLTHMPNQFNHDTODEAGLEVH 68
D 11 SLLAALLQSSGAAASAKELACOEITVPLCKGIGYNTYTMPOFNHDTODEAGLEVH 70
QY 69 QFWPLVEIQCSFDLRFPLCTMTPTICLPDYHAKPLPPCSVCERAAAGSPLMROYGFAMP 128
D 71 QFWPLVEIQCSFDLRFPLCSMTPTICLEDYKKPLPPCRSVCERAAAGCAPLMROYGFAMP 130
QY 129 ERMSCDRLPVIGRAAEVYCMQYNRSBATTA---PPRPPAKPTLPG-----PPG 174
D 131 DRMRCDRLPEQG-NPDTLCMDYNRTDLTTAAPSPPRLPPP--PGEOPPSGSGHGRPPG 187
QY 175 A-----PASGG-----ECPAGGPFV-----CKREPFVPIIKESH 205
D 188 ARPHRGGGSGGGGDAAPAPARGGGGKARPPGGGAAPCEPGQCCRAPMVSVSSERHP 247
QY 206 LYNKRTGQVNCAPVCPQPSFSADERTF 234
D 248 LYNKRTGQIANCALPCHNPFPSODERAF 276
```

RESULT 5

```
US-10-285-976-53
Sequence 53, Application US/10285976
GENERAL INFORMATION:
APPLICANT: Rhee, Chae-Seo
APPLICANT: Malini, Sen
APPLICANT: Wu, Christina
APPLICANT: Leonil, Lorenzo M.
APPLICANT: Corti, Mariapat
APPLICANT: Carson, Dennis A.
TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
TITLE OF INVENTION: In Head and Neck Squamous Cell Carcinomas
FILE REFERENCE: 023070-130320US
CURRENT APPLICATION NUMBER: US/10/285,976
PRIOR FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US 60/287,995
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: WO PCT/US02/13802
NUMBER OF SEQ ID NOS: 232
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 53
LENGTH: 694
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human frizzled8 (Fzd8)
US-10-285-976-53
```

```
Query Match          62.9%; Score 824; DB 6; Length 694;
Best Local Similarity 59.9%; Pred. No. 5.2e-54;
Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;
```

```
QY 11 SLL--LTLIAQLVGRAAAAKAPVCOEITVPMCRGIGYNTLTHMPNQFNHDTODEAGLEVH 68
D 11 SLLAALLQSSGAAASAKELACOEITVPLCKGIGYNTYTMPOFNHDTODEAGLEVH 70
QY 69 QFWPLVEIQCSFDLRFPLCTMTPTICLPDYHAKPLPPCRSVCERAAAGSPLMROYGFAMP 128
```

```
Db 71 QFWPLVEIQCSFDLRFPLCSMTPTICLEDYKKPLPPCRSVCERAAAGCAPLMROYGFAMP 130
QY 129 ERMSCDRLPVIGRAAEVYCMQYNRSBATTA---PPRPPAKPTLPG-----PPG 174
D 131 DRMRCDRLPEQG-NPDTLCMDYNRTDLTTAAPSPPRLPPP--PGEOPPSGSGHGRPPG 187
QY 175 A-----PASGG-----ECPAGGPFV-----CKREPFVPIIKESH 205
D 188 ARPHRGGGSGGGGDAAPAPARGGGGKARPPGGGAAPCEPGQCCRAPMVSVSSERHP 247
QY 206 LYNKRTGQVNCAPVCPQPSFSADERTF 234
D 248 LYNKRTGQIANCALPCHNPFPSODERAF 276
```

RESULT 6

```
US-10-115-678-250
Sequence 250, Application US/10115678
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Wang, Yonghong
APPLICANT: Weng, Gezhi
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Xue, Aidong J.
APPLICANT: Wang, Jian-Rui
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Malabika
APPLICANT: Wang, Duntui
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Secreted Polypeptides
FILE REFERENCE: 805ACON
CURRENT APPLICATION NUMBER: US/10/115,678
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 10/112,944
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/306,971
PRIOR FILING DATE: 2001-07-21
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SOFTWARE: pt_genes Version 5.0
SEQ ID NO 250
LENGTH: 694
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION:
US-10-115-678-250
```

```
Query Match          62.9%; Score 824; DB 6; Length 694;
Best Local Similarity 59.9%; Pred. No. 5.2e-54;
Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;
```

```
QY 11 SLL--LTLIAQLVGRAAAAKAPVCOEITVPMCRGIGYNTLTHMPNQFNHDTODEAGLEVH 68
D 11 SLLAALLQSSGAAASAKELACOEITVPLCKGIGYNTYTMPOFNHDTODEAGLEVH 70
```

OY	69	QFWPLVEI:QCSPDLRFELCTMYTTPCLSDYHKKPLPCQCSVERKAKGCSPLYMRGYAMP	128
Dd	71	QFWPLVEI:QCSPDLRFELCTMYTTPCLSDYHKKPLPCQCSVERKAKGCAAPLMROYGAMP	130
OY	129	BRMSCDRLPVLGRDAVLCMDYNRSEATTA---PPRPFAKTLPFG-----PPG	174
Dd	131	DRMRCDDLPEQG-NBDTLQMDYNRDLTTAAISPFRLLPRPP-PSGQPSGSCHGRPG	187
OY	175	A-----PASGG-----ECPAGEFV---CKGREPVFLKSHSHP	205
Dd	188	AAPRRGGGCGGGGDAAAAPARGGGGGGKARPPGGGAAPCEGCOCRAFPVSVSSERHP	247
OY	206	LYNRYVTGQVPNCAYVCYQPSFSABERTF	234
Dd	248	LYNRYVTGQIANCALPCINPFPSODERAFF	276

RESULT 7
US-10-112-944-250

Query Match 62.9%; Score 824; DB 6; Length 694;
 Best Local Similarity 59.9%; Pred. No. 5.2e-54;
 Matches 161; Conservative 21; Mismatches 39; Indels 48; Gaps 8;

[illegible]

```

RESULT 8
US-60-452-680-21108
; Sequence 21108, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 21108
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-21108

```

Query Match	62.9%	Score 824	DB 7	Length 694
Best Local Similarity	59.9%	Pred. No. 5.2e-54		
Matches 161	Conservative	21	Mismatches 39	Indels 48
				Gaps 8

QY	11	SLT--LLLLAQVGRGAAASKAPVCCITVPCRCIGNYLTMHPNQFNHDTDEAGLEVH	68
DB	11	SLTAAALLQRSSGAAASAKELAQELITVPCCKIGNYTMTMPQFNHDTDEAGLEVH	70
QY	69	QFWPLVEIQCSDDLRFCTMYTPICLBDYHKPLPCRSVCERAKAGCSPLMRQYGFAMP	128
DB	71	QWPLVEIQCSDDLRFCTMYTPICLBDYKXPLPCRSVCERAKAGCAPLMRQYGFAMP	130
QY	129	EMNSCDRLPVLGRDAEVLCTMDYNRSEATTA--PRPRPAKPTLPG-----PPG	174
DB	131	DMRCDRLPEQG--NPDITCMQDYNRDLTTAASPFRRLPPPE--PGEOPSSGSHGRPPG	187
QY	175	A-----PASGG-----ECPRGGPFV-----CKCREPFLIKESH	205
DB	188	APRPHRGGRGGGGDAAPAPRGGGGGGGAKAPPGGGAACPCEPGQCQCAPVSVSERRP	247
QY	206	LYNKVKTGQVPCNCAVPCYQPSFADERTF	234
DB	248	LYNKVKTGQIANCALPCNNPFPSQERRAP	276

```

RESULT 9
US-10-301-764-14
; Sequence 14, Application US/10301764
; GENERAL INFORMATION:
; APPLICANT: Umaneky, Samuil
; Melkonyan, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA

```

COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,764
FILING DATE: 20-Nov-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 685 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-301-764-14

Query Match 62.9%; Score 823.5; DB 6; Length 685;
Best Local Similarity 60.0%; Pred. No. 5,66-54;
Matches 159; Conservative 24; Mismatches 39; Indels 43; Gaps 8;
QY 11 SIL--LLLAQLVGRGAASAKAPVCOEITVPMCRGIGYVLTMPNQFNHDTODEAGLEVH 68
DB 11 SILAALAVLGRSSGAASAKELACOEITVPLCKIGYVYTMPNQFNHDTODEAGLEVH 70
QY 69 QFWPLVEIQCSDDLRFELCTWYTPICLPDYHKPLPRCSVCERAKAGCSPLMRQGFAMP 128
DB 71 QFWPLVEIQCSDDLRFELCSMTTPICLEDYKPLPRCSVCERAKAGCAPLMRQGFAMP 130
QY 129 ERMSCDRLVLRGDAVLCMDYNRSEATTA---PPRPPAKPTLPG-----PPG 174
DB 131 DRMRCDRLPEQG-NPDTLCMDYNRDTLTAAPSPPRLPPPP--PGEQPPSGSGHRRPG 188
QY 175 A-----PASGEC--PAGGPFV---CKREPFVPILESHP 209
DB 189 ARPPHGGSSRSGDAAAPAPRGCGKARPPGGAAPCEBGCOCRAAPMVSVSESRHPLVNR 248
QY 210 VRTGOVNCVPCYQPSFSADERTF 234
DB 249 VKTGOIANCALPCNHPFSQDERAF 273

RESULT 10
US-10-264-825-38
Sequence 38, Application US/10264825
GENERAL INFORMATION:
APPLICANT: He, Biao
APPLICANT: You, Liang
APPLICANT: Xu, Zhidong
APPLICANT: Jiaobion, David M.
TITLE OF INVENTION: Methods for Treating Cancer by
Inhibiting Wnt Signalling
FILE REFERENCE: 023070-125600US
CURRENT APPLICATION NUMBER: US/10/264,825
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 38
LENGTH: 275

TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)-(275)
OTHER INFORMATION: human Frizzled-8 peptide sequence
US-10-264-825-38

Query Match 62.4%; Score 818; DB 6; Length 275;
Best Local Similarity 59.9%; Pred. No. 6,76-54;
Matches 160; Conservative 21; Mismatches 38; Indels 48; Gaps 8;

QY 11 SIL--LLLAQLVGRGAASAKAPVCOEITVPMCRGIGYVLTMPNQFNHDTODEAGLEVH 68
DB 11 SILAALAVLGRSSGAASAKELACOEITVPLCKIGYVYTMPNQFNHDTODEAGLEVH 70
QY 69 QFWPLVEIQCSDDLRFELCTWYTPICLPDYHKPLPRCSVCERAKAGCSPLMRQGFAMP 128
DB 71 QFWPLVEIQCSDDLRFELCSMTTPICLEDYKPLPRCSVCERAKAGCAPLMRQGFAMP 130
QY 129 ERMSCDRLVLRGDAVLCMDYNRSEATTA---PPRPPAKPTLPG-----PPG 174
DB 131 DRMRCDRLPEQG-NPDTLCMDYNRDTLTAAPSPPRLPPPP--PGEQPPSGSGHRRPG 187
QY 175 A-----PASGEC--PAGGPFV---CKREPFVPILESHP 205
DB 189 ARPPHGGSSRSGDAAAPAPRGCGGKARPPGGAAPCEBGCOCRAAPMVSVSESRHPLVNR 247
QY 206 LYNKVRTGOVNCVPCYQPSFSADERTF 232
DB 248 LYNRVKTGOIANCALPCNHPFSQDERAF 274

RESULT 11
US-10-301-764-8
Sequence 8, Application US/10301764
GENERAL INFORMATION:
APPLICANT: Melkonian, Samuel
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,764
FILING DATE: 20-Nov-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 565 amino acids
TYPE: amino acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-10-301-764-8

Query Match 36.4%; Score 477; DB 6; Length 565;
 Best Local Similarity 41.9%; Pred. No. 4,8e-28;
 Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;

QY 3 RDPSPAPSLILLILLLAQLVGRMAAASKAPV-----COEITVPMCRGIGYNLTMPNOF 55
 Db 2 RRSALPRLILLPLLLPAAGPAQFHGEKGISIPDHGFCQPSISPLCTDIAYNTIMPNI 61
 QY 56 NHDTOEAGLEVHQFWPLVEIQCSPLRFFLCMTYTPICLPDYHKPLPPCRSVCERAKAG 115
 Db 62 GHTNODAGLEVHQFVPLVKVQCSPLRFFLCMTYTPICLPDYHKPLPPCRSVCERAKAG 120
 QY 116 CSPLMRQYGFAMPERMSCDRLPVLGRDAEVLCDYNRSE-----ATTAPRRFPFA-KPT 168
 Db 121 CEALMNRKFGFQWPERLRCHEHFRHG--AEQICVGNHSEBDGAPALLTTAP--PGLQPG 175
 QY 169 LGPPAPASGEGCPAGG----PFVCKCREPVPILKESHPLYNKVRGTQGVNCAVPCVQ 224
 Db 176 AGTTPGGGGGAPPRYATLEHFFHCP-----RVLKV--PSYLSYKFLGERDCAAPC-E 226
 QY 225 PS-----FSADERTFA 235
 Db 227 PARPDGSMFSGQETRF 244

RESULT 12
 US-10-225-567A-382
 Sequence 382, Application US/10225567A

GENERAL INFORMATION:
 APPLICANT: Lifespan Biosciences
 APPLICANT: Brown, Joseph P.
 APPLICANT: Burner, Glenna C.
 APPLICANT: Roush, Christine L.
 TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 FILE REFERENCE: 1920-4-4
 CURRENT APPLICATION NUMBER: US/10/225,567A
 CURRENT FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 60/257,144
 PRIOR FILING DATE: 2000-12-19
 NUMBER OF SEQ ID NOS: 2292
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 382
 LENGTH: 565
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-225-567A-382

Query Match 36.4%; Score 477; DB 6; Length 565;
 Best Local Similarity 41.9%; Pred. No. 4,8e-28;
 Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;

QY 3 RDPSPAPSLILLILLLAQLVGRMAAASKAPV-----COEITVPMCRGIGYNLTMPNOF 55
 Db 2 RRSALPRLILLPLLLPAAGPAQFHGEKGISIPDHGFCQPSISPLCTDIAYNTIMPNI 61
 QY 56 NHDTOEAGLEVHQFWPLVEIQCSPLRFFLCMTYTPICLPDYHKPLPPCRSVCERAKAG 115
 Db 62 GHTNODAGLEVHQFVPLVKVQCSPLRFFLCMTYTPICLPDYHKPLPPCRSVCERAKAG 120
 QY 116 CSPLMRQYGFAMPERMSCDRLPVLGRDAEVLCDYNRSE-----ATTAPRRFPFA-KPT 168
 Db 121 CEALMNRKFGFQWPERLRCHEHFRHG--AEQICVGNHSEBDGAPALLTTAP--PGLQPG 175
 QY 169 LGPPAPASGEGCPAGG----PFVCKCREPVPILKESHPLYNKVRGTQGVNCAVPCVQ 224
 Db 176 AGTTPGGGGGAPPRYATLEHFFHCP-----RVLKV--PSYLSYKFLGERDCAAPC-E 226

QY 225 PS-----FSADERTFA 235
 Db 227 PARPDGSMFSGQETRF 244

RESULT 13
 US-10-285-976-41
 Sequence 41, Application US/10285976

GENERAL INFORMATION:
 APPLICANT: Rhee, Chae-Seo
 APPLICANT: Malini, Sen
 APPLICANT: Wu, Christina
 APPLICANT: Leonil, Lorenzo M.
 APPLICANT: Corr, Maripat
 APPLICANT: Carson, Dennis A.
 TITLE OF INVENTION: The Regents of the University of California
 TITLE OF INVENTION: In Head and Neck Squamous Cell Carcinomas
 FILE REFERENCE: 023070-130320US
 CURRENT APPLICATION NUMBER: US/10/285,976
 CURRENT FILING DATE: 2002-11-01
 PRIOR APPLICATION NUMBER: US 60/287,995
 PRIOR FILING DATE: 2001-05-01
 PRIOR APPLICATION NUMBER: WO PCT/US02/13802
 PRIOR FILING DATE: 2002-05-01
 NUMBER OF SEQ ID NOS: 232
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 41
 LENGTH: 565
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: human frizzled2 (Fzd2)
 US-10-285-976-41

Query Match 36.4%; Score 477; DB 6; Length 565;
 Best Local Similarity 41.9%; Pred. No. 4,8e-28;
 Matches 108; Conservative 31; Mismatches 79; Indels 40; Gaps 11;

QY 3 RDPSPAPSLILLILLLAQLVGRMAAASKAPV-----COEITVPMCRGIGYNLTMPNOF 55
 Db 2 RRSALPRLILLPLLLPAAGPAQFHGEKGISIPDHGFCQPSISPLCTDIAYNTIMPNI 61
 QY 56 NHDTOEAGLEVHQFWPLVEIQCSPLRFFLCMTYTPICLPDYHKPLPPCRSVCERAKAG 115
 Db 62 GHTNODAGLEVHQFVPLVKVQCSPLRFFLCMTYTPICLPDYHKPLPPCRSVCERAKAG 120
 QY 116 CSPLMRQYGFAMPERMSCDRLPVLGRDAEVLCDYNRSE-----ATTAPRRFPFA-KPT 168
 Db 121 CEALMNRKFGFQWPERLRCHEHFRHG--AEQICVGNHSEBDGAPALLTTAP--PGLQPG 175
 QY 169 LGPPAPASGEGCPAGG----PFVCKCREPVPILKESHPLYNKVRGTQGVNCAVPCVQ 224
 Db 176 AGTTPGGGGGAPPRYATLEHFFHCP-----RVLKV--PSYLSYKFLGERDCAAPC-E 226
 QY 225 PS-----FSADERTFA 235
 Db 227 PARPDGSMFSGQETRF 244

RESULT 14
 US-60-453-9598
 Sequence 9598, Application US/60453135

GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele
 APPLICANT: TAKUBOVA, Olga
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001456
 CURRENT APPLICATION NUMBER: US/60/453,135
 CURRENT FILING DATE: 2003-03-10
 NUMBER OF SEQ ID NOS: 82762
 SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9598
LENGTH: 563
TYPE: PRT
ORGANISM: Homo sapiens
US-60-453-135-9598

Query Match 36.1%; Score 472.5; DB 7; Length 563;
Best Local Similarity 42.7%; Pred. No. 1.1e-27;
Matches 109; Conservative 30; Mismatches 75; Indels 41; Gaps 12;

QY 7 SAPSLLL-LLLAQLVGRRAAASKAPV-----COEITVPMCRGIGYNLTMPNQFNHD 58
DB 3 SALPRLLLPRLLPAAQPAQHFGEKGISIPDHGFCQPIISIPCTDIAYNQTIMPNLGH 62
QY 59 TODEAGLEVHQWFWPLVEIQSPDLRFLLCTMTYPTICLPDYHKLPPCRSVCRAXAGCSP 118
DB 63 NOEDAGLEVHQWFWPLVKVQCSPELRFLLCSMYAPVCTV-LEQAIPPCRSICERAROGCEA 121
QY 119 LMRQYGFAMPERMSCDRLVLCGRDAEVLCDYNRSE-----ATTAPRRPFA-KPTLPG 171
DB 122 LMNKGFGQWPERLRCEHFRHG--AEQICVGQNHSEGDAPALLTTAP--PGLQPGAGG 176
QY 172 PPGAPASGGECPAGG---PFVCKCREPFVPIKESHPLYNKVRGQVNCAPVCYOPS- 226
DB 177 TFGGFGGAGAPRYATLEHFRHCP-----RVLKV--PSYLSYKFLGERDCAAPC-EPAR 227
QY 227 -----FSADERTFA 235
DB PDGSMFFSQEETRFA 242

RESULT 15
US-60-453-050-9598
Sequence 9598. Application US/60453050
GENERAL INFORMATION:
APPLICANT: CARCILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001457
CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9598
LENGTH: 563
TYPE: PRT
ORGANISM: Homo sapiens
US-60-453-050-9598

Query Match 36.1%; Score 472.5; DB 7; Length 563;
Best Local Similarity 42.7%; Pred. No. 1.1e-27;
Matches 109; Conservative 30; Mismatches 75; Indels 41; Gaps 12;

QY 7 SAPSLLL-LLLAQLVGRRAAASKAPV-----COEITVPMCRGIGYNLTMPNQFNHD 58
DB 3 SALPRLLLPRLLPAAQPAQHFGEKGISIPDHGFCQPIISIPCTDIAYNQTIMPNLGH 62
QY 59 TODEAGLEVHQWFWPLVEIQSPDLRFLLCTMTYPTICLPDYHKLPPCRSVCRAXAGCSP 118
DB 63 NOEDAGLEVHQWFWPLVKVQCSPELRFLLCSMYAPVCTV-LEQAIPPCRSICERAROGCEA 121
QY 119 LMRQYGFAMPERMSCDRLVLCGRDAEVLCDYNRSE-----ATTAPRRPFA-KPTLPG 171
DB 122 LMNKGFGQWPERLRCEHFRHG--AEQICVGQNHSEGDAPALLTTAP--PGLQPGAGG 176
QY 172 PPGAPASGGECPAGG---PFVCKCREPFVPIKESHPLYNKVRGQVNCAPVCYOPS- 226
DB 177 TFGGFGGAGAPRYATLEHFRHCP-----RVLKV--PSYLSYKFLGERDCAAPC-EPAR 227
QY 227 -----FSADERTFA 235
DB PDGSMFFSQEETRFA 242

Search completed: May 19, 2003, 16:43:09
Job time : 94 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 22, 2003, 21:14:04 ; Search time 2410 Seconds
(without alignments)
2451.653 Million cell updates/sec

Title: US-09-847-102a-68

Perfect score: 1310

Sequence: 1 MARDPSPAPSLILLALLAQL.....PNCAPVPCYQPSFADERTFA 235

Scoring table: BLOSUM62
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
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SUMMARIES

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3	1310	100.0	2334	15	US-09-107-112-3
4	1310	100.0	2334	41	US-10-152-548-9
5	1310	100.0	2334	45	US-60-015-307-9
6	1306	99.7	3124	64	US-60-207-360-77


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Qy 201 LysGusSerHisProLeuTyrAsnLysValArgThrGlyGlnValProAsnCysAlaVal 220
Db 921 AAGAGTACACACCCCTCTACACAAGGTGGCGGCGGAGTCCCACTGCGCGGTA 980
Qy 221 ProCysTyrGlnProSerPheSerHisAlaAspGluArgThrPheAla 235
Db 981 CCTCTACTACAGCCGCTCTTCAAGTGCAGCGAGCGACGTTGCGC 1025

RESULT 2
US-09-053-375B-1495
; Sequence 1495, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilaehvilli, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1495
; LENGTH: 2334
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-053-375B-1495

Alignment Scores:
Pred. No.: 2 01e-73 Length: 2334
Score: 1310.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-847-102a-68 (1-235) x US-09-053-375B-1495 (1-2334)
Qy 1 MetAlaArgProAspProSerHisAlaProProSerLeuLeuLeuLeuAlaGlnLeu 20
Db 321 ATGGCTCGGCGCTGACCACTGACGCGCGGCGCTGCTGCTGCTGCTGCGGAGCTG 380
Qy 21 ValGlyArgAlaAlaAlaAlaSerLysAlaProValCysGlnGluIleThrValProMet 40
Db 381 GTGGGCGCGGCGCGCGCGCTGCAAGGCGCGGTGTGTCAGGAATCAAGGCGCCATG 440
Qy 41 CysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
Db 441 TCCCGGGGATGGGCTACCACTGACGACATGCCCCAACCAGTTCAACACAGACAGCAG 500
Qy 61 AspGluAlaGlyLeuGluValHisGlnPheTyrProLeuValGluIleGlnCysSerPro 80
Db 501 GACGAGGCGGCGCTGAGAGTGCACCAAGTCTGCGCGCTGTGAGATTCCAATGCTGCGG 560
Qy 81 AspLeuArgPhePheLeuCysThrMetTyrThrProIleCysLeuProAspTyrHisLys 100
Db 561 GACCTGCGCTTCTTCTATGCACTATGTAACGCGCATCTGTCTGCCAGTACCAAG 620
Qy 101 ProLeuProProCysArgSerValCysGluArgAlaLysAlaGlyCysSerProLeuMet 120
Db 621 CCGCTGCGCGCTGCGCTGCGGTGTGTCAGCGGCGGCGGCGGCTGCTGCGCTGAGT 680
Qy 121 ArgGlnTyrGlyPheAlaTyrProGluArgMetSerCysAspArgLeuProValLeuGly 140
Db 681 CCGCAGTAGGCTTCCGCTGCGCGCGGCGGCGGAGTGTGAGTCCGCTCCGCTGCTGGG 740
Qy 141 ArgAspAlaGlyValLeuCysMetAspTyrAsnArgSerGluAlaThrAlaProPro 160
Db 741 CCGCAGCGCGAGGTCTCTGCACTGATTAACCGGACGAGGCGACACGCGGCGCCCC 800
Qy 161 ArgProPheProAlaLysProThrLeuProGlyProProGlyValAlaProLysArgGly 180
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Qy 181 GluCysProAlaGlyGlyProPheValCysLysCysAlaGluProPheValProIleLeu 200
Db 861 GAATGCCCCGCTGGGGGCGCCCTTCTGTGCAAGTGTCCGAGCCCTTGTGCTTCTG 920
Qy 201 LysGusSerHisProLeuTyrAsnLysValArgThrGlyGlnValProAsnCysAlaVal 220
Db 921 AAGAGTACACACCCCTCTACACAAGGTGGCGGCGGAGTCCCACTGCGCGGTA 980
Qy 221 ProCysTyrGlnProSerPheSerHisAlaAspGluArgThrPheAla 235
Db 981 CCTCTACTACAGCCGCTCTTCAAGTGCAGCGAGCGACGTTGCGC 1025

RESULT 3
US-09-107-112-3
; Sequence 3, Application US/09107112
; GENERAL INFORMATION:
; APPLICANT: Morin, Peter
; APPLICANT: Kosik, Kenneth S.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR TREATING ALZHEIMER'S DISEASE
; FILE REFERENCE: 05311/020001
; CURRENT APPLICATION NUMBER: US/09/107,112
; CURRENT FILING DATE: 1998-06-30
; EARLIER APPLICATION NUMBER: US 60/051,359
; EARLIER FILING DATE: 1997-06-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2334
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (321)...(2075)
US-09-107-112-3

Alignment Scores:
Pred. No.: 2 01e-73 Length: 2334
Score: 1310.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-847-102a-68 (1-235) x US-09-107-112-3 (1-2334)
Qy 1 MetAlaArgProAspProSerHisAlaProProSerLeuLeuLeuLeuAlaGlnLeu 20
Db 321 ATGGCTCGGCGCTGACCACTGACGCGCGGCGCTGCTGCTGCTGCTGCGGAGCTG 380
Qy 21 ValGlyArgAlaAlaAlaAlaSerLysAlaProValCysGlnGluIleThrValProMet 40
Db 381 GTGGGCGCGGCGCGCGCGCTGCAAGGCGCGGTGTGTCAGGAATCAAGGCGCCATG 440
Qy 41 CysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
Db 441 TCCCGGGGATGGGCTACCACTGACGACATGCCCCAACCAGTTCAACACAGACAGCAG 500
Qy 61 AspGluAlaGlyLeuGluValHisGlnPheTyrProLeuValGluIleGlnCysSerPro 80
Db 501 GACGAGGCGGCGCTGAGAGTGCACCAAGTCTGCGCGGTGTGAGATTCCAATGCTGCGG 560
Qy 81 AspLeuArgPhePheLeuCysThrMetTyrThrProIleCysLeuProAspTyrHisLys 100
Db 561 GACCTGCGCTTCTTCTATGCACTATGTAACGCGCATCTGTCTGCCAGTACCAAG 620
Qy 101 ProLeuProProCysArgSerValCysGluArgAlaLysAlaGlyCysSerProLeuMet 120
Db 621 CCGCTGCGCGCTGCGCTGCGGTGTGTCAGCGGCGGCGGCGGCTGCTGCGCTGAGT 680
Qy 121 ArgGlnTyrGlyPheAlaTyrProGluArgMetSerCysAspArgLeuProValLeuGly 140
Db 681 CCGCAGTAGGCTTCCGCTGCGCGCGGCGGCGGAGTGTGAGTCCGCTCCGCTGCTGGG 740

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QY 141 ArgaspAlaGluValIleuCySerMetAspTyrAsnArgSerGluAlaThrThrAlaProPro 160
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 QY 161 ArgProPheProAlaIleuProThrIleuProGlyProProGlyAlaProAlaSerGlyGly 180
 Db 801 AGGCTTTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 860
 QY 181 GluCyProAlaGlyIleuProPheValCysIleuCyArgGluProPheValProIleu 200
 Db 861 GAATGCCCGCGTGGGGGCGCTTCTGCTGCAAGTGTCCGAGCCCTTCGTCCTCATTCTG 920
 QY 201 LysGluSerHisProLeuTyrAsnIleuValArgThrGlyGluValProAsnCysAlaVal 220
 Db 921 AAGAGTCAACCCGCTTACAAACAAGTGGCGAGCGCGAGCTGCCAATCGCGGTA 980
 QY 221 ProGlyTyrGluProSerPheSerAlaAspGluArgThrPheAla 235
 Db 981 CCTGCTACAGCCGCTTCACTGAGTGGAGAGCGAGCGAGCTTCCGC 1025

RESULT 4 US-10-152-548-9

Sequence 9, Application US/10152548
 GENERAL INFORMATION:
 APPLICANT: Bhanot, Purnima

Brink, Marcel
 Harryman, Cindy S.
 Wang, Yanshu
 Hsieh, Jen-chih
 Andrew, Deborah
 Nathans, Jeremy
 Nusse, Roel

TITLE OF INVENTION: Wnt Receptor Compositions and Methods
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/152,548
 FILING DATE: 21-May-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/832,340
 FILING DATE: 11-APR-1997
 APPLICATION NUMBER: US 60/015,307
 FILING DATE: 12-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: 38,615
 REFERENCE/DOCKET NUMBER: 8600-0167.30
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2334 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Human transmembrane receptor

SEQUENCE DESCRIPTION: SEQ ID NO: 9: (Frazzled 5) mRNA, Coding region: 321..2078
 US-10-152-548-9

Alignment Scores:
 Pred. No.: 2,01e-73 Length: 2334
 Score: 1310.00 Matches: 235
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 41 Gaps: 0

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QY 1 MetAlaArgProAspProSerSerAlaProProSerLeuLeuLeuLeuAlaGlnLeu 20
 Db 321 ARGGCTCGGCTGAGCCATCCGCGCGCTTCTGCTGCTGCTGCTGCTGCGGAGCTG 380
 QY 21 ValGlyArgAlaAlaAlaAlaSerIleValaProValCysGlnGluIleThrValProMet 40
 Db 381 GTGGCGCGGCGCGCGCGCGCTCAAGGCGCGGTGTGCGAAGAAATCAGGCTGCCAAG 440
 QY 41 CysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
 Db 441 TCCCGCGGATCGGCTGACCACTGAGCAGCATGCGCCACAGTTCACACACAGCAGCAG 500
 QY 61 AspGluAlaGlyLeuGluValHisGlnPheThrProLeuValGluIleGlnCysSerPro 80
 Db 501 GACGAGCGCGGCGCTGAGAGTGCACCATTCGCGCGCTGTGGAGATTCACATGCTCGCGG 560
 QY 81 AspleuArgPhePheLeuCySerThrMetCysThrThrProIleCysLeuProAspTyrHisIlys 100
 Db 561 GACCTGCGCTTCTTCAATGACATGATGACAGCCCATCTGCTGCCACTACACCAAG 620
 QY 101 ProIleuProProCysArgSerValCysGluArgAlaIleValCysSerProLeuMet 120
 Db 621 CCGCTGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 680
 QY 121 ArgGlnTyrGlyPheAlaThrProGluArgMetSerCysAspArgLeuProValIleuGly 140
 Db 681 CCGGAGTACGCTTGGCTGCGCGCGCGAGCGCATGAGCTGAGCCGCTCCGCGTGGCGG 740
 QY 141 ArgaspAlaGluValIleuCySerMetAspTyrAsnArgSerGluAlaThrThrAlaProPro 160
 Db 741 CCGGAGCGCGAGGTCTCTGATGATTAACAACCGAGCGAGCGACCAAGCGCGCCCC 800
 QY 161 ArgProPheProAlaIleuProThrIleuProGlyProProGlyAlaProAlaSerGlyGly 180
 Db 801 AGGCTTTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 860
 QY 181 GluCyProAlaGlyIleuProPheValCysIleuCyArgGluProPheValProIleu 200
 Db 861 GAATGCCCGCGTGGGGGCGCTTCTGCTGCAAGTGTCCGAGCCCTTCGTCCTCATTCTG 920
 QY 201 LysGluSerHisProLeuTyrAsnIleuValArgThrGlyGluValProAsnCysAlaVal 220
 Db 921 AAGAGTCAACCCGCTTACAAACAAGTGGCGAGCGCGAGCTGCCAATCGCGGTA 980
 QY 221 ProGlyTyrGluProSerPheSerAlaAspGluArgThrPheAla 235
 Db 981 CCTGCTACAGCCGCTTCACTGAGTGGAGAGCGAGCGAGCTTCCGC 1025

RESULT 5 US-60-015-307-9

Sequence 9, Application US/60015307
 GENERAL INFORMATION:

APPLICANT: Bhanot, Purnima
 APPLICANT: Brink, Marcel
 APPLICANT: Harryman, Cindy S.
 APPLICANT: Wang, Yanshu
 APPLICANT: Hsieh, Jen-chih
 APPLICANT: Andrew, Deborah
 APPLICANT: Nathans, Jeremy

QY 101 ProleuProProCysArgSerValCysGluValAlaLysAlaGlyCysSerProleuMet 120
 DB 847 CCGCTCCCGCCCGCTCGGTGCTGAGCGCGCCAGCGCGCTGCTGCGCGCTGATG 906
 QY 121 ArgGlnTyrGlyPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuGly 140
 DB 907 CGGCACTACGGCTTCCCTGCGCGCGCGCGATGAGCTGGACCTCCCGGTGCTGGG 966
 QY 141 ArgAspAlaGluValLeuCysMetAspTyrAsnArgSerGluAlaThrThrAlaProPro 160
 DB 967 CGGAGCGCGAGGCTCTGTCATGATTCACACCGAGAGGCGCACACGCGCGCCCC 1026
 QY 161 ArgProPheProAlaLysProThrLeuProGlyProProGlyAlaProAlaSerGlyGly 180
 DB 1027 AGGCTCTTCCAGCCAGCCCAAGCCCTTCCAGGCGCGCGCGCGCGCGCGCGG 1086
 QY 181 GluCysProAlaGlyGlyProPheValCysLysCysArgGluProPheValProleu 200
 DB 1087 GAATGCCCCGCTGGGGGCGCGCTGCTGTCAGTGTGCGAGCGCTTCTGCTGCTG 1146
 QY 201 LysGluSerHisProLeuTyrAsnLysValArgThrGlyGlnValProAsnCysAlaVal 220
 DB 1147 AAGGAGTCAACACCGCTCTACACAGTGGCGAGCGCGCGCGCGCGCGCGCGG 1206
 QY 221 ProCysTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
 DB 1207 CCTGCTACAGCCGCTCTTCAAGTCCGAGCGAGCGCGCGCTTCCG 1251

RESULT 7

US-60-129-391-1913
 ; Sequence 1913, Application US/60129391
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith et al.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN THE DIAGNOSIS AND TREATMENT C
 ; FILE REFERENCE: 107196, 138
 ; CURRENT APPLICATION NUMBER: US/60/129,391
 ; NUMBER OF SEQ ID NOS: 1999-04-13
 ; SEQ ID NO 1913
 ; LENGTH: 2555
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1), (2552), (2553), (2554), (2555)
 ; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno
 US-60-129-391-1913

Alignment Scores:

Pred. No.: 6,13e-71 Length: 2555
 Score: 1271.50 Matches: 232
 Percent Similarity: 99.15% Conservative: 1
 Best Local Similarity: 98.72% Mismatches: 1
 Query Match: 97.06% Indels: 2
 DB: 56 Gaps: 1

US-09-847-102a-68 (1-235) x US-60-129-391-1913 (1-2555)

QY 1 MetAlaArgProAspProSerAlaProProSerLeuLeuLeuLeuLeuLeuAlaGlnLeu 20
 DB 383 ATGGCTCGGCGCTGACCATCCGCGCGCGCTCGCTGCTGCTGCTGCGCGAGCTG 442
 QY 21 ValGluArgAlaAlaAlaAlaSerLysAlaProValCysGlnGluLeuThrValPromet 40
 DB 443 GTGGCGCGGCGCGCGCGCGCTCAAGGC-CCG---TGCAGGAATTCACGGTGGCCATG 498
 QY 41 CysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
 DB 499 TGGCGGCGGATGGCTACCAACCTGACGACATGCCCAACAGTTCAACACGACGAGCG 558
 QY 61 AspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGluIleGlnCysSerPro 80

DB 559 GACGAGCGGCGCTGAGAGTGCACCAATTCCTGCGCGCTGCGAGATCCATGCTCCGCC 618
 QY 81 AspLeuArgPhePheLeuCysThrMetTyrThrProIleCysLeuProAspTyrHisLys 100
 DB 619 GACCTGGCGCTTCTCTATGCTCTATGATACAGGCCCATCTGCTGCCGACTACCAAG 678
 QY 101 ProleuProProCysArgSerValCysGluValAlaLysAlaGlyCysSerProleuMet 120
 DB 679 CGGCTCGCGCTTCCCTGCGCTGCTGTCAGGCGCGCGCGCGCGCGCGCGCGCTG 738
 QY 121 ArgGlnTyrGlyPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuGly 140
 DB 739 CCGGATACGCTTCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 798
 QY 141 ArgAspAlaGluValLeuCysMetAspTyrAsnArgSerGluAlaThrThrAlaProPro 160
 DB 799 CGGAGCGCGAGGCTCTGTCATGATTCACACCGAGAGGCGCACACGCGCGCCCC 858
 QY 161 ArgProPheProAlaLysProThrLeuProGlyProProGlyAlaProAlaSerGlyGly 180
 DB 859 AGGCTTTCAGCCAGCCAGCCCAAGCCCTTCCAGGCGCGCGCGCGCGCGCGCG 918
 QY 181 GluCysProAlaGlyGlyProPheValCysLysCysArgGluProPheValProleu 200
 DB 919 GAATGCCCCGCTGGGGGCGCGCTGCTGTCAGTGTGCGAGCGCTTCTGCTGCTG 978
 QY 201 LysGluSerHisProLeuTyrAsnLysValArgThrGlyGlnValProAsnCysAlaVal 220
 DB 979 AAGGAGTCAACACCGCTCTACACAGTGGCGAGCGCGCGCGCGCGCGCGCGG 1038
 QY 221 ProCysTyrGlnProSerPheSerAlaAspGluArgThrPheAla 235
 DB 1039 CCTGCTACAGCCGCTCTTCAAGTCCGAGCGAGCGCGCGCGCTTCCG 1083

RESULT 8

US-60-360-207-18143
 ; Sequence 18143, Application US/60360207
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig
 ; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
 ; FILE REFERENCE: CL001321
 ; CURRENT APPLICATION NUMBER: US/60/360,207
 ; NUMBER OF SEQ ID NOS: 2002-03-01
 ; SEQ ID NO 18143
 ; LENGTH: 1758
 ; TYPE: DNA
 ; ORGANISM: HUMAN
 US-60-360-207-18143

Alignment Scores:

Pred. No.: 9,73e-70 Length: 1758
 Score: 1250.00 Matches: 224
 Percent Similarity: 97.02% Conservative: 4
 Best Local Similarity: 95.32% Mismatches: 7
 Query Match: 95.42% Indels: 0
 DB: 80 Gaps: 0

US-09-847-102a-68 (1-235) x US-60-360-207-18143 (1-1758)

QY 1 MetAlaArgProAspProSerAlaProProSerLeuLeuLeuLeuLeuLeuAlaGlnLeu 20
 DB 1 ATGGCTCGACCGGACCGCTGCGCGCTCTCTCTCTGCTGCTGCTGCTGCGAGCTG 60
 QY 21 ValGluArgAlaAlaAlaAlaSerLysAlaProValCysGlnGluLeuThrValPromet 40
 DB 61 GTGGCGCGGCGAGCGCGCGCTCAAGGCGCGGCTGTCAGGAATTCACGGTGGCCATG 120
 QY 41 CysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
 DB 121 TCCGAGGCGATGGCTACCACTGACGACATGCCCAACCACTTCAACCATACACGAG 180
 QY 61 AspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGluIleGlnCysSerPro 80

Db 181 GACGAGGAGGCTGAGAGTGCACCAATTCGTGGCGCTTGAGATCACTGACTCAGC 240
Qy 81 AspleuAcgPhePheLeuCyethrmetTyrThrProileCysLeuProaspTyrhislys 100
Db 241 GACCTGCGCTTCTTCTGCTGCTATGACAGCCCACTGTTTGCTGACTACACAG 300
Qy 101 ProleuProProCyAargserValCysgluAargValaLysaglyCysserProleumet 120
Db 301 CCGCTACACAGCGGTCCGTTCGCTGCGAGCGCCAGGCGCGGTGCTGCGCGCTCATG 360
Qy 121 ArggluTyrGlyPheAlaIleProgluAargmetserCysAspArgLeuProValleuGly 140
Db 361 CGCAGTACGCGCTTCTGCTGCGCTGCGAGCGAGCAGCTGCGAGCGCTGCTGCTGAGC 420
Qy 141 ArgAspAlaGluValleuCyethrmetAspTyrAsnaArgserGluAlaThrThrAlaProPro 160
Db 421 GCGGAGCGCGAGGCTTCTGCTGCTATGATTAACCAAGAGCAACCAACCGCGCTCCCT 480
Qy 161 ArgProPheProAlaLysProThrleuProgluProProgluValaProAlaSerGlyGly 180
Db 481 AAGTCTTCCGCGCAAACTCACTCCAGAGACCAACGAGGCGCGCTTCCGCGGAGC 540
Qy 181 GluCyProAlaGlyGlyProPheValCyslysCysArgGluProPheValProileu 200
Db 541 GAGTCCCTCGGAGGCGCCATCCGTGTCAGCTGCGCGAGCCCTGCTGCTGCTGCTG 600
Qy 201 LysGluSerHisProLeuTyrAsnLysValArgThrGlyGluValProAsnCysAlaVal 220
Db 601 AAGGAGTACACCACTCTTACACAAAGTGCAGCGCGGCAAGTCCCACTGCGCGGTG 660
Qy 221 ProCyTyrGluProSerPheSerAlaAspGluArgThrPheAla 235
Db 661 CCTCTACACAGCGCTTCTTCAAGCGCGAGCGCAACTTGCC 705

RESULT 9

US-60-229-515-1423
; Sequence 1423, Application US/60229515
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000776
; CURRENT APPLICATION NUMBER: US/60/229,515
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1423
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: HUMAN
US-60-229-515-1423

Alignment Scores:

Pred. No.: 5,4e-68 Length: 1630
Score: 1222.00 Matches: 217
Percent Similarity: 100.00% Conservatve: 1
Best Local Similarity: 99.54% Mismatches: 0
Query Match: 93.28% Indels: 0
DB: 66 Gaps: 0

US-09-847-102a-68 (1-235) x US-60-229-515-1423 (1-1630)

Qy 18 AlaGluLeuValGlyArgAlaAlaAlaSerLysAlaProValCysGluGluIleThr 37
Db 3 GCGCAGCTGCTGCGCGCGCGCGCGCGCGCTCAAGCGCGCTGCTGCGAGAAATCAAG 62
Qy 38 ValPrometCysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHis 57
Db 63 GTGCCCATGTGCGCGCGCATCGCTACAACTCGAAGCAGACATCCCAACAGTTCAACAC 122
Qy 58 AspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGluIleGln 77

Db 123 GACAGCGAGAGGAGCGGCGCTGAGGTGCACCAAGTTCGCTGCTGAGATCCAA 182
Qy 78 CysSerProAspLeuArgPhePheLeuCyethrmetTyrThrProileCysLeuProasp 97
Db 183 TGCTGCGGAGACTGCGCTTCTTCTGCTATGACAGCCCACTGCTGCTGCTGAGC 242
Qy 98 TyrHisLysProLeuProProCyAargserValCysgluAargValaLysaglyCysSer 117
Db 243 TACCAAGAGCGGTGCGCGCTGCGGTGCTGCGAGCGCGCGCAAGCGCGGTGCTG 302
Qy 118 ProleuMetArgGluTyrGlyPheAlaIleProgluAargmetserCysAspArgLeuPro 137
Db 303 CCGCTGAGCGCGAGTACGAGCTTCTGCTGCGCGCGAGCAGATGAGCTGAGCGCTCCG 362
Qy 138 ValLeuGlyArgAspAlaGluValleuCyethrmetAspTyrAsnaArgserGluAlaThrThr 157
Db 363 GTCTGCGGCGCGAGCGCGAGGCTCTCTGCTATGATTAACCAAGAGCAACCGAGCGCAC 422
Qy 158 AlaProProArgProPheProAlaLysProThrleuProgluProProgluValaProAla 177
Db 423 GCGCGCGCGAGCGCTTCCAGCGCAAGCCCTTCCAGGCGCGCGCGCGCGCGCG 482
Qy 178 SerGlyGlyGluCyProAlaGlyGlyProPheValCyslysCysArgGluProPheVal 197
Db 483 TCGGCGGCGAGATGCCGCTGCGGCGCGCGCTTCTGCTGCTGCTGCTGCTG 542
Qy 198 ProileuLysGluSerHisProLeuTyrAsnLysValArgThrGlyGluValProAsn 217
Db 543 CCTCTGAGAGGATCACACCGCTCTTACAAAGTGCAGCGCGGCAAGTCCCACTGCGCG 602
Qy 218 CysAlaValProCyTyrGluProSerPheSerAlaAspGluArgThrPheAla 235
Db 603 TCGCGGATACCTGCTGACACCGCTTCAAGTGCAGCGAGCGGACGTTGCG 656

RESULT 10

US-60-213-169-11
; Sequence 11, Application US/60213169
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, ELLEN
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000699
; CURRENT APPLICATION NUMBER: US/60/213,169
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 678
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 785
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(785)
; OTHER INFORMATION: n = A,T,C or G
US-60-213-169-11

Alignment Scores:

Pred. No.: 2,87e-57 Length: 785
Score: 1048.00 Matches: 185
Percent Similarity: 95.90% Conservatve: 2
Best Local Similarity: 94.87% Mismatches: 8
Query Match: 80.00% Indels: 0
DB: 65 Gaps: 0

US-09-847-102a-68 (1-235) x US-60-213-169-11 (1-785)

Qy 41 CysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
Db 11 TCGACAGCTGAGGTTCTACTCTAGNAGAGATCCCAACAGTTCAACAGACAGGAG 70
Qy 61 AspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGluIleGlnCysSerPro 80

```
Db 71 GACGAGGCGGCGCTGAGGTGCAACGAGGCGCTGCTGAGATCCAAATGCTGCGCG 130
QY 81 AAPLeuArpPhePheLeuCyThrmTyTrPProIleCySLeuProAspTyTrHisLys 100
Db 131 GACCTGGCTTTCTTCTATGCTTATGTAACAGCCCATCTGTGTGCCAGTACACACAAG 190
QY 101 ProLeuProProCySArgSerValCysGluArgAlaLysAlaGlyCysSerProLeuMet 120
Db 191 CCGCTGCGCGCTGCGCTGCGGTGTCGAGCGCGCCAGCGCGCGCTGCTGCGCGCTGCTG 250
QY 121 ArgGlnTyGlyPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuGly 140
Db 251 CCGCAGTACGCGCTTCCCTGCGCGCCGAGCCCATGAGTGTGCGACCGCTCCCGGTGCTGGCG 310
QY 141 ArgAspAlaGluValLeuCySmetAspTyTrAsnArgSerGluAlaThrThrAlaProPro 160
Db 311 CCGAGCGCGAGGTCTCTGTCATGATTAACACGAGCGAGCGACACGAGCGCGCGCC 370
QY 161 ArgProPheProAlaLysProThrLeuProGlyProProGlyValaProAlaSerGlyGly 180
Db 371 AGGCTTTCCAGCCAGCCAGCCACCTTCCAGCGCGCGCGCGCGCGCTGCGGCGCG 430
QY 181 GluCySPROAlaGlyGlyProPheValCysLysCysArgGluProPheValProIleLeu 200
Db 431 GAATGCCCCGCTGGGGCGCGCTTCTGTGCAAGTGTGCGAGCGCTTCTGCGCCATTCTG 490
QY 201 LysGluSerHisProLeuTyTrAsnLysValaArgThrGlyGlnValaProAsnCySAlaVal 220
Db 491 AAGGAGTCAACACCGCTCTTACACAGGTGCGAGCGAGCGAGTGTGCGCGCGCG 550
QY 221 ProCySTyGlnProSerPheSerAlaAspGluArgThrPheAla 235
Db 551 CCTGTACACGCGCTTCTTCAAGTGTGCGAGCGAGCGACGCTTGTGCC 595
```

```
RESULT 11
US-60-213-170-11
; Sequence 11, Application US/60213170
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, ELLEN
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO00699
; CURRENT APPLICATION NUMBER: US/60/213,170
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 678
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 785
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(785)
; OTHER INFORMATION: n = A,T,C or G
US-60-213-170-11
```

```
Alignment Scores:
Pred. No.: 2,87e-57 Length: 785
Score: 1048.00 Matches: 185
Percent Similarity: 95.90% Conservative: 2
Best Local Similarity: 94.87% Mismatches: 8
Query Match: 80.00% Indels: 0
DB: Gaps: 0
```

US-09-847-102a-68 (1-235) x US-60-213-170-11 (1-785)

```
QY 41 CysArgGlyIleGlyTyTrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln 60
Db 11 TGCAGACCTGCGAGGTCTACTACTAGAGAGATCCCCCAACAGTTCACACGACGACGAG 70
QY 61 AspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGluIleGlnCysSerPro 80
```

```
Db 71 GACGAGGCGGCGCTGAGGTGCAACGAGGCGCTGCTGAGATCCAAATGCTGCGCG 130
QY 81 AAPLeuArpPhePheLeuCyThrmTyTrPProIleCySLeuProAspTyTrHisLys 100
Db 131 GACCTGGCTTTCTTCTATGCTTATGTAACAGCCCATCTGTGTGCCAGTACACACAAG 190
QY 101 ProLeuProProCySArgSerValCysGluArgAlaLysAlaGlyCysSerProLeuMet 120
Db 191 CCGCTGCGCGCTGCGCTGCGGTGTCGAGCGCGCCAGCGCGCGCTGCTGCGCGCTGCTG 250
QY 121 ArgGlnTyGlyPheAlaTrpProGluArgMetSerCysAspArgLeuProValLeuGly 140
Db 251 CCGCAGTACGCGCTTCCCTGCGCGCCGAGCCCATGAGTGTGCGACCGCTCCCGGTGCTGGCG 310
QY 141 ArgAspAlaGluValLeuCySmetAspTyTrAsnArgSerGluAlaThrThrAlaProPro 160
Db 311 CCGAGCGCGAGGTCTCTGTCATGATTAACACGAGCGAGCGACACGAGCGCGCGCC 370
QY 161 ArgProPheProAlaLysProThrLeuProGlyProProGlyValaProAlaSerGlyGly 180
Db 371 AGGCTTTCCAGCCAGCCAGCCACCTTCCAGCGCGCGCGCGCGCGCTGCGGCGCG 430
QY 181 GluCySPROAlaGlyGlyProPheValCysLysCysArgGluProPheValProIleLeu 200
Db 431 GAATGCCCCGCTGGGGCGCGCTTCTGTGCAAGTGTGCGAGCGCTTCTGCGCCATTCTG 490
QY 201 LysGluSerHisProLeuTyTrAsnLysValaArgThrGlyGlnValaProAsnCySAlaVal 220
Db 491 AAGGAGTCAACACCGCTCTTACACAGGTGCGAGCGAGCGAGTGTGCGCGCGCG 550
QY 221 ProCySTyGlnProSerPheSerAlaAspGluArgThrPheAla 235
Db 551 CCTGTACACGCGCTTCTTCAAGTGTGCGAGCGAGCGACGCTTGTGCC 595
```

```
RESULT 12
US-60-213-169-463
; Sequence 463, Application US/60213169
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, ELLEN
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO00699
; CURRENT APPLICATION NUMBER: US/60/213,169
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 678
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 463
; LENGTH: 696
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(696)
; OTHER INFORMATION: n = A,T,C or G
US-60-213-169-463
```

```
Alignment Scores:
Pred. No.: 3,66e-55 Length: 696
Score: 1014.00 Matches: 178
Percent Similarity: 99.45% Conservative: 2
Best Local Similarity: 98.34% Mismatches: 1
Query Match: 77.40% Indels: 0
DB: Gaps: 0
```

US-09-847-102a-68 (1-235) x US-60-213-169-463 (1-696)

```
QY 55 PheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheTrpProLeuVal 74
Db 2 TTCACACAGACACACGAGAGCGAGCGCGCTGAGAGTGCACACAGAGGCGCGCTGG 61
QY 75 GluIleGlnCysSerProAspLeuArgPhePheLeuCyThrmTyTrThrProIleCys 94
```

```
Db 62 GAGATCCAAATGCTCGCCGAGACCTGGCGCTTCTTCTATGCTCTATGACCGCCATCTGT 121
Qy 95 LeuProAspTYRHILysPProLeuProProCyAsrSerValCySGluArgAlaLysAla 114
Db 122 CTGCCGCACTACACAAAGCCGCTGCGCCCTGCGTGTGCGAGCGCCCAAGGCC 181
Qy 115 GilySerProLeuMeuArgGlnTyrGilyPheAlaTTPProGluArgMetSerCyAsp 134
Db 182 GCGCTCGCGCGCTGCGTGGCCAGTACGGCTTGGCTGGCCGAGCGCATGAGCTGGCAG 241
Qy 135 ArgLeuProValLeuGilyArgAspAlaGluValLeuCyMetAspTyrAsnArgSerGlu 154
Db 242 GCGCTCGCGTGTGGCGCGAGCCGAGGTCCTCTGATGATTAACAACGCGAGCGG 301
Qy 155 AlaThrThrAlaProProArgProPheProAlaLysProThrLeuProGlyProProGly 174
Db 302 GCCACACAGCGCGCCCGCCAGGCTTCCAGCCAAAGCCACCTTCCAGCGCCGCAAGG 361
Qy 175 AlaProAlaSerGilyGilyGilyCySProAlaGilyGilyProPheValCyLysCyAspArgGlu 194
Db 362 GCGCGCGCTCGGGGGGGGGAATGCCCGCTGGGGGGCGCTTGCTGTGCAAGTGTGCGAG 421
Qy 195 ProPheValProIleLeuLysGlySerHisPProLeuTyrAsnLysValArgThrGlyGln 214
Db 422 CCTTCGTCGCCATTCGAAAGAGTACACCGCTCTACAAAGGTGGAGCGGGCCAG 481
Qy 215 ValProAsnCyAlaValAlaProCySerTyrGlnProSerPheSerAlaAspGluArgThrPhe 234
Db 482 GTGCCCAATGCGCGGTACCTGCTACCAAGCCGCTTCAAGTGTGCGAGCGGACGTTTC 541
Qy 235 Ala 235
Db 542 GCC 544
```

RESULT 13

```
US-60-213-170-463
; Sequence 463, Application US/60213170
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, ELLEN
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO00699
; CURRENT APPLICATION NUMBER: US/60/213,170
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 678
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 463
; LENGTH: 696
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(696)
; OTHER INFORMATION: n = A,T,C or G
US-60-213-170-463
```

Alignment Scores:

```
Pred. No.: 3,666-55 Length: 696
Score: 1014.00 Matches: 178
Percent Similarity: 99.45% Conservative: 2
Best Local Similarity: 98.34% Mismatches: 1
Query Match: 77.40% Indels: 0
DB: Gaps: 0
```

US-09-847-102a-68 (1-235) x US-60-213-170-463 (1-696)

```
Qy 55 PheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHisGlnPheThrProLeuVal 74
Db 2 TTCACACAGCAAGCAGCAGGCGGCTGAGAGTGCACACAGGAGGCGCGCTGGG 61
Qy 75 GtIleGlnCySerProAspLeuArgPhePheLeuCyThrMetTyrThrProIleCyS 94
```

```
Db 62 GAGATCCAAATGCTCGCCGAGACCTGGCGCTTCTTCTATGCTCTATGACCGCCATCTGT 121
Qy 95 LeuProAspTYRHILysPProLeuProProCyAsrSerValCySGluArgAlaLysAla 114
Db 122 CTGCCGCACTACACAAAGCCGCTGCGCCCTGCGTGTGCGAGCGCCCAAGGCC 181
Qy 115 GilySerProLeuMeuArgGlnTyrGilyPheAlaTTPProGluArgMetSerCyAsp 134
Db 182 GCGCTCGCGCGCTGCGTGGCCAGTACGGCTTGGCTGGCCGAGCGCATGAGCTGGCAG 241
Qy 135 ArgLeuProValLeuGilyArgAspAlaGluValLeuCyMetAspTyrAsnArgSerGlu 154
Db 242 GCGCTCGCGTGTGGCGCGAGCCGAGGTCCTCTGATGATTAACAACGCGAGCGG 301
Qy 155 AlaThrThrAlaProProArgProPheProAlaLysProThrLeuProGlyProProGly 174
Db 302 GCCACACAGCGCGCCCGCCAGGCTTCCAGCCAAAGCCACCTTCCAGCGCCGCAAGG 361
Qy 175 AlaProAlaSerGilyGilyGilyCySProAlaGilyGilyProPheValCyLysCyAspArgGlu 194
Db 362 GCGCGCGCTCGGGGGGGGGAATGCCCGCTGGGGGGCGCTTGCTGTGCAAGTGTGCGAG 421
Qy 195 ProPheValProIleLeuLysGlySerHisPProLeuTyrAsnLysValArgThrGlyGln 214
Db 422 CCTTCGTCGCCATTCGAAAGAGTACACCGCTCTACAAAGGTGGAGCGGGCCAG 481
Qy 215 ValProAsnCyAlaValAlaProCySerTyrGlnProSerPheSerAlaAspGluArgThrPhe 234
Db 482 GTGCCCAATGCGCGGTACCTGCTACCAAGCCGCTTCAAGTGTGCGAGCGGACGTTTC 541
Qy 235 Ala 235
Db 542 GCC 544
```

RESULT 14

```
US-60-177-646-1336/c
; Sequence 1336, Application US/60177646
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO00210
; CURRENT APPLICATION NUMBER: US/60/177,646
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 4226
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1336
; LENGTH: 611
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(611)
; OTHER INFORMATION: n = A,T,C or G
US-60-177-646-1336
```

Alignment Scores:

```
Pred. No.: 2,986-49 Length: 611
Score: 920.00 Matches: 162
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.38% Mismatches: 0
Query Match: 70.23% Indels: 0
DB: Gaps: 0
```

US-09-847-102a-68 (1-235) x US-60-177-646-1336 (1-611)

```
Qy 73 LeuValGluIleGlnCySerProAspLeuArgPhePheLeuCyThrMetTyrThrPro 92
Db 610 CTGGTGAAGATCCAAATGCTCGCCGAGACCTGGCGCTTCTTCTATGCTCTATGACCGCC 551
Qy 93 IleCyLeuProAspTYRHILysPProLeuProProCyAsrSerValCySGluArgAla 112
Db 550 ATCTGTCTGCCGCACTACACAGCCGCTGCGCCCTGCGTGTGCGAGCGCCGCG 491
Qy 113 LysAlaGilyCySerProLeuMeuArgGlnTyrGilyPheAlaTTPProGluArgMetSer 132
```

```

Db      490 AAGGCGGCTGCTCGCGCTGATGCGCCAGTACGGCTCGCCGCGCCGCGCATGAGC 431
QY      133 CysAspArgLeuProValIleuGIyArgAspAlaGluValIleuGlySerMetAspTyrAsnArg 152
Db      430 TGGACCGGCTCCCGGTGTGGGGCGGACGCCGAGAGCTCTTGCAATGATTAACAACCCG 371
QY      153 SerGluAlaThrThrAlaProProAlaProPheProAlaAlaAspProThrIleuProGlyPro 172
Db      370 AGGAGAGCCACACGCGCGCCGCCAGGCTTCCAGGCCACAGCCACCTTCCAGGCCCG 311
QY      173 ProGlyAlaProAlaSerGlyGIyGluCysProAlaGlyGlyProPheValCysIysCys 192
Db      310 CCAGGGGCGCCGCGCTCGGGGGGCGAATGCCCGCTGGGGGCGCGTTCGTGTGCAAGTGT 251
QY      193 ArgGluProPheValProIleuIysGluSerHisProLeuTyrAsnIysValArgThr 212
Db      250 CCGAGCCCTTCGTGTCATTCGAAGAGTCAACCCGCTTACAAACAAGGTGCGGAGCG 191
QY      213 GlyGluValProAsnCysAlaValProCysTyrGlnProSerPheSerAlaAspGluArg 232
Db      190 GCGCAGTGCCTCCCACTGCGCGGTAACCTGTACACCCGCTTCACTGAGTCCGACGAGCC 131
QY      233 ThrPheAla 235
Db      130 ACGTTCGCC 122

```

RESULT 15

```

US-60-178-308-1287/c
/ Sequence 1287, Application US/60178308
/ GENERAL INFORMATION:
/ APPLICANT: Bonazzi, Vivien
/ TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
/ TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
/ TITLE OF INVENTION: PROTEINS, AND USES THEREOF
/ FILE REFERENCE: CL000204
/ CURRENT APPLICATION NUMBER: US/60/178,308
/ CURRENT FILING DATE: 2000-01-27
/ NUMBER OF SEQ ID NOS: 344
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1287
/ LENGTH: 611
/ TYPE: DNA
/ ORGANISM: HUMAN
US-60-178-308-1287

```

Alignment Scores:

```

Pred. No.: 2,98e-49 Length: 611
Score: 920.00 Matches: 162
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.39% Mismatches: 0
Query Match: 70.23% Indels: 0
DB: 61 Gaps: 0

```

US-09-847-102a-68 (1-235) x US-60-178-308-1287 (1-611)

```

QY      73 LeuValGluIleGlnCysSerProAspLeuArgPhePheLeuGlyThrMetTyrThrPro 92
Db      610 CTGGTGAATCCAAATGCTGCGCGACTGCGGCTTCTCTTATGCTTATGATACACCCC 551
QY      93 IleCysLeuProAspTyrHisIysProLeuProProCysAspSerValCysGluArgAla 112
Db      550 ATCTGTCTGCGCGACTACCAACAAGCGCTGCGCGCTCGCGGTGCGGTGCGAGCGCGCC 491
QY      113 LysAlaGlyCysSerProLeuMetArgGlnTyrGlyPheAlaTrpProGluArgMetSer 132
Db      490 AAGGCGGCTGCTCGCGCTGAGCGCCAGTACGAGCTTCGCTGCGCCGCGAGCGCATGAGC 431
QY      133 CysAspArgLeuProValIleuGIyArgAspAlaGluValIleuGlySerMetAspTyrAsnArg 152
Db      430 TGGACCGGCTCCCGGTGTGGGGCGGACGCCGAGAGCTCTTGCAATGATTAACAACCCG 371
QY      153 SerGluAlaThrThrAlaProProAlaProPheProAlaAlaAspProThrIleuProGlyPro 172

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Db      370 AGCGAGGCCACACGCGCGCCGCCAGGCTTCCAGGCCAAGCCACCTTCCAGGCCCG 311
QY      173 ProGlyAlaProAlaSerGlyGIyGluCysProAlaGlyGlyProPheValCysIysCys 192
Db      310 CCAGGGGCGCCGCGCTCGGGGGGCGAATGCCCGCTGGGGGCGCGTTCGTGTGCAAGTGT 251
QY      193 ArgGluProPheValProIleuIysGluSerHisProLeuTyrAsnIysValArgThr 212
Db      250 CCGAGCCCTTCGTGTCATTCGAAGAGTCAACCCGCTTACAAACAAGGTGCGGAGCG 191
QY      213 GlyGluValProAsnCysAlaValProCysTyrGlnProSerPheSerAlaAspGluArg 232
Db      190 GCGCAGTGCCTCCCACTGCGCGGTAACCTGTACACCCGCTTCACTGAGTCCGACGAGCC 131
QY      233 ThrPheAla 235
Db      130 ACGTTCGCC 122

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Search completed: May 23, 2003, 04:40:15
Job time : 2430 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model.

Run on: May 22, 2003, 18:01:48 ; Search time 603 Seconds
(without alignments)
2021.442 Million cell updates/sec

Title: US-09-847-102a-68
Perfect score: 1310
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Searched: 6438716 seqs, 2593467500 residues
Total number of hits satisfying chosen parameters: 12877432

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Database : Pending Patents NA_New.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1310	100.0	2334	8	US-10-285-976-48
2	1306	99.7	2674	8	US-10-170-235-22610
3	1250	95.4	1758	9	US-10-144-771-18143
4	824	62.9	2085	9	US-10-311-623-18
5	824	62.9	3182	8	US-10-170-235-35769
6	824	62.9	3182	11	US-60-453-135-1905
7	824	62.9	3195	8	US-10-285-976-54

8	824	62.9	3206	8	US-10-115-678-6	Sequence 6, Appl1
9	824	62.9	3206	8 <td>US-10-112-944-6</td> <td>Sequence 6, Appl1</td>	US-10-112-944-6	Sequence 6, Appl1
10	823.5	62.9	2058	9 <td>US-10-144-771-1276</td> <td>Sequence 10276, A</td>	US-10-144-771-1276	Sequence 10276, A
11	479.5	36.6	2043	9 <td>US-10-144-771-12343</td> <td>Sequence 12343, A</td>	US-10-144-771-12343	Sequence 12343, A
12	477	36.4	1983	8 <td>US-10-285-976-42</td> <td>Sequence 42, Appl</td>	US-10-285-976-42	Sequence 42, Appl
13	477	36.4	1983	9 <td>US-10-225-567A-581</td> <td>Sequence 381, Appl</td>	US-10-225-567A-581	Sequence 381, Appl
14	472.5	36.1	1933	8 <td>US-10-170-235-13965</td> <td>Sequence 33965, A</td>	US-10-170-235-13965	Sequence 33965, A
15	472.5	36.1	1933	11 <td>US-60-453-135-1905</td> <td>Sequence 1905, Ap</td>	US-60-453-135-1905	Sequence 1905, Ap
16	472.5	36.1	1933	11 <td>US-60-453-135-1905</td> <td>Sequence 1905, Ap</td>	US-60-453-135-1905	Sequence 1905, Ap
17	472.5	36.1	211587	5 <td>US-09-948-128-281</td> <td>Sequence 281, Ap</td>	US-09-948-128-281	Sequence 281, Ap
18	461	35.2	3851	1 <td>PCT-US02-24567-26</td> <td>Sequence 26, Appl</td>	PCT-US02-24567-26	Sequence 26, Appl
19	461	35.2	3851	8 <td>US-10-285-976-52</td> <td>Sequence 52, Appl</td>	US-10-285-976-52	Sequence 52, Appl
20	461	35.2	3851	8 <td>US-10-210-120-26</td> <td>Sequence 26, Appl</td>	US-10-210-120-26	Sequence 26, Appl
21	440.5	33.6	2262	9 <td>US-10-144-771-16597</td> <td>Sequence 16597, A</td>	US-10-144-771-16597	Sequence 16597, A
22	417	31.8	1929	9 <td>US-10-144-771-691</td> <td>Sequence 691, Appl</td>	US-10-144-771-691	Sequence 691, Appl
23	415	31.7	4350	8 <td>US-10-285-976-40</td> <td>Sequence 40, Appl</td>	US-10-285-976-40	Sequence 40, Appl
24	415	31.7	4537	8 <td>US-10-170-235-18992</td> <td>Sequence 18992, A</td>	US-10-170-235-18992	Sequence 18992, A
25	406	31.0	4837	8 <td>US-10-062-674-1978</td> <td>Sequence 1978, Ap</td>	US-10-062-674-1978	Sequence 1978, Ap
26	399	30.5	2184	8 <td>US-10-285-976-56</td> <td>Sequence 56, Appl</td>	US-10-285-976-56	Sequence 56, Appl
27	399	30.5	2184	9 <td>US-10-342-887-920</td> <td>Sequence 920, Appl</td>	US-10-342-887-920	Sequence 920, Appl
28	399	30.5	2405	8 <td>US-10-170-235-19899</td> <td>Sequence 19899, A</td>	US-10-170-235-19899	Sequence 19899, A
29	398	30.4	4540	1 <td>PCT-US03-03194-3422</td> <td>Sequence 3422, Ap</td>	PCT-US03-03194-3422	Sequence 3422, Ap
30	398	30.4	4540	11 <td>US-60-436-643-3422</td> <td>Sequence 3422, Ap</td>	US-60-436-643-3422	Sequence 3422, Ap
31	394.5	30.1	1779	9 <td>US-10-144-771-46172</td> <td>Sequence 46172, A</td>	US-10-144-771-46172	Sequence 46172, A
32	388	29.6	2270	9 <td>US-10-017-161-799</td> <td>Sequence 799, Appl</td>	US-10-017-161-799	Sequence 799, Appl
33	387	29.5	658	8 <td>US-10-405-027-61</td> <td>Sequence 61, Appl</td>	US-10-405-027-61	Sequence 61, Appl
34	387	29.5	1746	1 <td>PCT-US02-41414-1522</td> <td>Sequence 1522, Ap</td>	PCT-US02-41414-1522	Sequence 1522, Ap
35	387	29.5	2811	1 <td>PCT-US02-41414-1521</td> <td>Sequence 1521, Ap</td>	PCT-US02-41414-1521	Sequence 1521, Ap
36	387	29.5	3254	8 <td>US-10-170-235-22704</td> <td>Sequence 22704, A</td>	US-10-170-235-22704	Sequence 22704, A
37	387	29.5	3260	8 <td>US-10-285-976-58</td> <td>Sequence 58, Appl</td>	US-10-285-976-58	Sequence 58, Appl
38	387	29.5	22804	1 <td>PCT-US02-41414-1520</td> <td>Sequence 1520, Appl</td>	PCT-US02-41414-1520	Sequence 1520, Appl
39	380.5	29.0	1909	4 <td>PCT-US02-41225A-203</td> <td>Sequence 203, Appl</td>	PCT-US02-41225A-203	Sequence 203, Appl
40	380.5	29.0	1909	5 <td>US-09-873-367C-282</td> <td>Sequence 282, Appl</td>	US-09-873-367C-282	Sequence 282, Appl
41	380	29.0	978	1 <td>PCT-US02-41225A-204</td> <td>Sequence 204, Appl</td>	PCT-US02-41225A-204	Sequence 204, Appl
42	372.5	28.4	1738	7 <td>US-09-948-016-1873</td> <td>Sequence 1873, Ap</td>	US-09-948-016-1873	Sequence 1873, Ap
43	372.5	28.4	2151	8 <td>US-10-170-235-6760</td> <td>Sequence 6760, Ap</td>	US-10-170-235-6760	Sequence 6760, Ap
44	372.5	28.4	2151	11 <td>US-60-453-135-4168</td> <td>Sequence 4168, Ap</td>	US-60-453-135-4168	Sequence 4168, Ap
45	372.5	28.4	2151	11 <td>US-60-453-050-4168</td> <td>Sequence 4168, Ap</td>	US-60-453-050-4168	Sequence 4168, Ap

ALIGNMENTS

RESULT 1
US-10-285-976-48
Sequence 48, Application US/10285976
GENERAL INFORMATION:
APPLICANT: Rhee, Chae-Seo
APPLICANT: Malini, Sen
APPLICANT: Wu, Christina
APPLICANT: Leon, Lorenzo M.
APPLICANT: Carr, Maripat
APPLICANT: Carson, Dennis A.
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Mt and Frizzled Receptors as Targets for Immunotherapy
FILE REFERENCE: 023070-130320US
CURRENT APPLICATION NUMBER: US/10/285,976
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US 60/287,995
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: WO PCT/US02/13802
PRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 232
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 48
LENGTH: 2334
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human frizzleds (Fzds)
US-10-285-976-48
Alignment Scores:

Pred. No.:	3,17e-80	Length:	233
Score:	1310.00	Matches:	235
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match..	100.00%	Indels:	0
DB:	8	Gaps:	0

US-09-847-102A-68 (1-235) x US-10-285-976-48 (1-2334)

Qy	1	MetAlaAqPProAspProSerAlaProProSerLeuLeuLeuLeuLeuAlaGlnLeu	20
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Qy	21	ValGlyAlaGalaAlaAlaAlaSerLysAlaProValCysGlnGluIleThrValPromet	40
Db	381	GTGGGCGCGGCGCGCGCGCTCCAGAGCCCCCGGGTGTCCAGGAATACAGTGGCCCATG	440
Qy	41	CysArgGlyIleGlyTyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln	60
Db	441	TGCGCGGCATCGGCTTACACCTGACGACACATGCCAACCGATTACACGACGACGCG	500
Qy	61	AspGlnAlaGlyLeuGlnValHisGlnPheTrpProLeuValGluIleGlnCysSerPro	80
Db	501	GACGAGCGGCGGCGCTGGAGGTGCACCAAGTTCTGCGCGCTGTGGAAATCCAATGCTCGCGG	560
Qy	81	AspLeuArgPhePheLeuCysThrMetTyrThrProIleCysIleuProAspTyrHisLys	100
Db	561	GACCTGCGCTTCTTCTATGACCTATGTACAGCCCATCTGTGCTCCGACCTACCAACAG	620
Qy	101	ProLeuProProCysArgSerValCysGlnArgAlaLysAlaGlyCysSerProLeuMet	120
Db	621	CGGTGCGCGCGCTGCGCTGCGGTGGGAGCGCGCCAGAGCGCGGTGCTCGCGCTGATG	680
Qy	121	ArgGlnTyrGlyPheAlaIleTrpProGluArgMetSerCysAspArgLeuProValLeuGly	140
Db	681	CGCCAGTACGGCTTCCTGCTGCGCCGAGGCGATGACCTCGACCGCTCCGATGCTGGGC	740
Qy	141	ArgAspAlaGluValLeuCysMetAspTyrAsnArgSerGluAlaThrThrAlaProPro	160
Db	741	CGCAGCGCGGAGGTCTCTGCAATGATTAACAACCGCACGAGGCCACACACGCGCGCCCC	800
Qy	161	ArgProPhePheProAlaLysProThrLeuProGlyProProGlyValaProAlaSerGly	180
Db	801	AGGCTTTCCTCCAGCCCAACCCCTTCCAGGCGCGCCAGGGGCGCCGCGCTCGGGGGGCG	860
Qy	181	GluCysProAlaGlyGlyProPheValCysLysCysArgGluProPheValProIleLeu	200
Db	861	GAAATCCCCGCTGGGGGCGCGCTTGTGTGCAAGTGTCCGAGACCTTGTGTGCCATTCTG	920
Qy	201	LysGlnSerHisProLeuTyrAsnLysValaArgThrGlyGlnValProAsnCysAlaVal	220
Db	921	AAGGAGTACACCCGCTTACAAACAAGGTGGCGAGCGGCGCAGGTGCCAACATCGCGGTGA	980
Qy	221	ProCysTyrGlnProSerPheSerAlaAspGluArgThrPheAla	235
Db	981	CCCTGCTACACCGCTCTTCAATGTCGACAGGCGCAGCGCTTGGC	1025

RESULT 2
US-10-170-235-22610
; Sequence 22610, Application US/10170235

1 APPLICANT: BENTON, J. C. Craig
 2 TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
 3 TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
 4 FILE REFERENCE: CL001380
 5 CURRENT APPLICATION NUMBER: US/10/170,235
 6 CURRENT FILING DATE: 2003-03-17
 7 NUMBER OF SEQ ID NOS: 42514
 8 SEQ ID NO 22610

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; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-22610

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Percent Similarity:	100.00%
Best Local Similarity:	99.57%
Query Match:	99.65%
DB:	8
Gaps:	0
Length:	267
Matches:	234
Conservative:	1
Mismatches:	0
Indels:	0

US-09-847-102A-68 (1-235) X US-10-170-235-22610 (1-2674)

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Qy	21	ValGlyArgAlaAlaAlaAlaSerLeuAlaProValCysGlnGlu1IleThrValPromet	40
Db	542	GTGGGCGGGGGCGCGCGCGCTCCAAAGCCCCGGGTGTGTCAGAAATCAACGGTGGCCATG	601
Qy	41	CysArgGlyIleGlyIlyrAsnLeuThrHisMetProAsnGlnPheAsnHisAspThrGln	60
Db	602	TGCGGGGCGATCGGCTTCAACCTTACCGCATGCCCCAACCGATTCAACACGACGCGNG	661
Qy	61	AspGluAlaGlyLeuGluValHisGlnPheTrpProLeuValGluIleGlnCysSerPro	80
Db	662	GACGAGCGGGCCCTGGAGAGTCAACAGTTCTGGCCGCTGGAGATCCAATGCTCGCCG	721
Qy	81	AspLeuArgPhePheLeuCysThrMetTyrThrProIleCysIleuProAspTyrHisIlys	100
Db	722	GACCTGGCGTTCTTCCATGCTCATGATGACGGCCCATCTTCTGCCCCGACTACCAACAG	781
Qy	101	ProLeuProProCysArgSerValCysGluArgAlaIlyAlaIyAlaGlyCysSerProLeuMet	120
Db	782	CCGCTGGCGCCCTGCGCGCTGGTGTGGAGCGCGCAAGGCCGGCTGTCGGCTGATG	841
Qy	121	ArgGlnTyrGlyPheAlaIleTrpProGluArgMetSerCysAspArgLeuProValIleuGly	140
Db	842	CGCAGATACGGCTTCGCTGGCCGAGCGCATGAGCTGCACCGGCTCCGGTGTGGGC	901
Qy	141	ArgAspAlaGluValLeuCysMetAspTyrAsnArgSerGluAlaThrThrAlaProPro	160
Db	902	CGCAGCCCGCAGGCTCTCTGATGATTACACCGCAGCAGGCCACACACGGCGCCCC	961
Qy	161	ArgProPheProAlaIyAlaProThrLeuProGlyProProGlyAlaProAlaSerGlyGly	180
Db	962	AGGCTTTTCCAGCGCAAGCCACCTTCACAGGCCCGCCAGGGGGCGCCGGCTCGGGGGGC	1022
Qy	181	GluCysProAlaGlyGlyProPheValCysIysCysArgGluProPheValProIleLeu	200
Db	1022	GAAATGCCCGCTGGGGGGCCGCTGTGTGTGCAAGTGTCCGACAGCCCTTGTGCCCATTTCTG	108
Qy	201	LysGluSerHisProLeuTyrAsnLysValArgThrGlyGlnValProAsnCysAlaVal	220
Db	1082	AAGAGATCACACCCGCTCTCAACAAGAGTGGGAGCGGCCACAGTGCACATGCGCGGTA	1144
Qy	221	ProCysTyrGlnProSerPheSerAlaAspGluArgThrPheAla	235
Db	1142	CCCTGCTACCAAGCCGCTCTTAGTGCAGACAGCGCAAGTTTCGCC	1186

RESULT 3
US-10-144-771-18143
; Sequence 18143, Application US/10144771

? APPLICANT: VENTER, J. Craig
 ? TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
 ? FILE REFERENCE: CL001321
 ? CURRENT APPLICATION NUMBER: US/10/144,771
 ? CURRENT FILING DATE: 2002-05-15
 ? NUMBER OF SEQ. ID NOS: 47235

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; LENGTH: 1758
; TYPE: DNA
; ORGANISM: HUMAN

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Db 271 ATGTACAGCCCATCTGCTAGAGACTTCAAGAACCGCTGCGCCGCTGCGCTGCGG 330
Qy 109 CysGluArgAlaValAlaGlyCysSerProleuMetArgIshlyGlyPheAlaTrpPro 128
Db 331 TCCGAGCGCGCCAGAGCCGCTGCGCGCGCTCATGCGCAGTACCGGCTTCCGTCGCGCC 390
Qy 129 GluArgMetSerCysAspArgLeuProValLeuGluArgAspAlaGluValLeuCysMet 148
Db 391 GACCGCATCGCTGCGAGCCGCTGCGCGCGCTGCGAGCAAGC---AACCTGACACGCTGTGCATG 447
Qy 149 AspTyrrhAsnArgSerGluAlaThrThrAla-----ProProArgProPheProAla 165
Db 448 GACTCAACACCGACCGACTTAACACCGCGCGCCAGCGCGCGCGCGCGCTGCGCGCG 507
Qy 166 LysProThrLeuProGly-----ProProGly 174
Db 508 CCGCGC-----CCCGCGAGCAGCGCCTTCCGCGAGCGCGCCAGCGCGCGCGCG 561
Qy 175 Ala----- 175
Db 562 GCCAGGCCCCCGACCG 621
Qy 176 ProAlaSerGlyGly-----GluCysProAlaGlyGlyProPheVal 189
Db 622 CCAAGCTCG 681
Qy 190 -----CysLysCysArgGluProPheValProIleuLysGluSerHisPro 205
Db 682 TCCGAGCG 741
Qy 206 LeuTyrrhAsnLysValArgThrGlyGlnValProAsnCysAlaValProCysTyrrhGlnPro 225
Db 742 CTCTCAACCGCGGTCAAGACAGCGCCAGATCGCTAACTGCGCGCTGCGCGCGCGCGCG 801
Qy 226 SerPheSerAlaAspGluArgThrPhe 234
Db 802 TTTTTCAGCCAGAGACGAGCGCGCTTC 828
RESULT 7
US-10-285-976-54
; Sequence 54, Application US/10285976
; GENERAL INFORMATION:
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Malini, Sen
; APPLICANT: Wu, Christina
; APPLICANT: Leonl, Lorenzo M.
; APPLICANT: Cori, Maridat
; APPLICANT: Carson, Dennis A.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
; FILE REFERENCE: In Head and Neck Squamous Cell Carcinomas
; CURRENT APPLICATION NUMBER: US/10285,976
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/287,995
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: WO PCT/US02/13802
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 3195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human frizzled8 (Fzd8)
US-10-285-976-54
Alignment Scores:

Pred. No.: 8.5e-47 Length: 3195
Score: 824.00 Matches: 161
Percent Similarity: 67.66% Conservative: 21
Best Local Similarity: 59.85% Mismatches: 39
Query Match: 52.90% Indels: 48
DB: 8 Gaps: 8
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Qy 11 SerLeuLeu-----LeuLeuLeuValGluValGlyArgAlaAlaAlaSer 28
Db 36 TCGCTGCTGCGCGCTTGGCGCTGCTGCGAGCGCTTACGCGCGCGCGCGCGCGCGCG 95
Qy 29 LysAlaProValGlyGluGluIshlyThrValProMetCysArgGlyIshlyTyrrhAsnLeu 48
Db 96 AAGAGCTGCGATGCGCAAGATCAACCGTGCCTGTGTAAAGGCGATCGCTCAACATAC 155
Qy 49 ThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHis 68
Db 156 ACCTACATGCGCCAAATCAAGTTCAACACACAGACAGCAAGAGCGCGCGCTGAGGTGCAC 215
Qy 69 GluPheTrpProLeuValGluIshlyGlnCysSerProAspLeuArgPheLeuCysThr 88
Db 216 CAGTTCTGCGCGCTGCTGAGATCCAGTCTGCGCGCGCTGCGATTCAGTTCTTCTGTCAGC 275
Qy 89 MetTyrrhProileCysLeuProAspTyrrhIshlyProleuProCysArgSerVal 108
Db 276 ATGTACAGCCCATCTGCTAGAGACTTCAAGAACCGCGCTGCGCGCGCGCGCTGCGGTG 335
Qy 109 CysGluArgAlaValAlaGlyCysSerProleuMetArgIshlyGlyPheAlaTrpPro 128
Db 336 TCCGAGCG 395
Qy 129 GluArgMetSerCysAspArgLeuProValLeuGluArgAspAlaGluValLeuCysMet 148
Db 336 GACCGCATCGCTGCGAGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 452
Qy 149 AspTyrrhAsnArgSerGluAlaThrThrAla-----ProProArgProPheProAla 165
Db 453 GACTCAACACCGACCGACTTAACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 512
Qy 166 LysProThrLeuProGly-----ProProGly 174
Db 513 CCGCGC-----CCCGCGAGCAGCGCCTTCCGCGAGCGCGCGCGCGCGCGCGCG 566
Qy 175 Ala----- 175
Db 567 GCCAGGCCCCCGACCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 626
Qy 176 ProAlaSerGlyGly-----GluCysProAlaGlyGlyProPheVal 189
Db 627 CCAAGCTCG 686
Qy 190 -----CysLysCysArgGluProPheValProIleuLysGluSerHisPro 205
Db 687 TCCGAGCGCGCGGTCAAGTGCAGCGCGCTATGCTGAGCGCTTCCAGAGCGCGCACCG 746
Qy 206 LeuTyrrhAsnLysValArgThrGlyGlnValProAsnCysAlaValProCysTyrrhGlnPro 225
Db 747 CTCTCAACCGCGGTCAAGACAGCGCCAGATCGCTAACTGCGCGCTGCGCGCGCGCGCG 806
Qy 226 SerPheSerAlaAspGluArgThrPhe 234
Db 807 TTTTTCAGCCAGAGACGAGCGCGCTTC 833
RESULT 8
US-10-115-678-6
; Sequence 6, Application US/10115678
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Gezhi
; APPLICANT: Zhang, Jie

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APPLICANT: Ren, Feiyun
APPLICANT: Xue, Aidong J.
APPLICANT: Wang, Jian-Rui
APPLICANT: Weinman, Tom
APPLICANT: Ghosh, Malabika
APPLICANT: Wang, Dunru
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Secreted Polypeptides
FILE REFERENCE: 805ACON
CURRENT APPLICATION NUMBER: US/10/115,678
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 10/112,944
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/306,971
PRIOR FILING DATE: 2001-07-21
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SOFTWARE: pc_Fl_Genes Version 5.0
SEQ ID NO 6
LENGTH: 3206
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (381)..(2462)
US-10-115-678-6

Alignment Scores:
Pred. No.: 8,53e-47 Length: 3206
Score: 824.00 Matches: 161
Percent Similarity: 67.66% Conservative: 39
Best Local Similarity: 59.85% Mismatches: 39
Query Match: 62.90% Indels: 48
DB: 8 Gaps: 8

US-09-847-102A-68 (1-235) x US-10-115-678-6 (1-3206)
OY 11 SerLeuLeu-----LeuLeuLeuLeuAlaGlnLeuValGlyValGAlaAlaAlaSer 28
Db 411 TCGGTGTCGGCCCGCTTGCGCGCTGCGCGCCCTTAAGGGGGGCGCGCGCGCTCGGCC 470
OY 29 LysAlaProValCysGlnGlnIleThrValProMetCysArgGlyIleGlyTyrAsnLeu 48
Db 471 AAGAGCTGGCAGTCCAGAGATCAACCGCGCTGTGTGAAGGGATCGGCTACAACTAC 530
OY 49 ThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHis 68
Db 531 ACCTACATGCGCAATCAATCAACCAACGACGCAAGACGAGCGCGGCTGAGGTGCAC 590
OY 69 GlnPheTyrProLeuValGlnIleGlnCysSerProAspLeuValGphePheLeuCysThr 88
Db 591 CAGTTCTGCGCGCTGTGGAGATCCAGTGTCTCGCCCGATCTCAAGTCTTCTCTGTGAC 650
OY 89 MetTyrThrProIleCysLeuProAspTyrHisIlePProLeuProProCysArgSerVal 108
Db 651 ATGACACGCCCATCTGCTCAAGAGCTVACAAGAACCGCGCTGCGCGCTGCGCTCGGTG 710

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Oy	109	CysGluArGAlaValSAIAGLVCysSerProLeuMetAArgIInTYRGI ¹ PhellaItrPro	128
Db	711	TGCAGACGCGCCAAAGCGCGCTGCGCGCCCTCATGCGCCAGTACGCGCTTGCGCTGCC	770
Oy	129	GIuArGMetSerCYcSAsPArgLeuProValIleuGIyArGAsPAlaGIuValIleuCYsMet	148
Db	771	GACCGCATGCGCTCGAGCGCGCTGCGCCAGCAAGGC---AACCCTGACACGCTGTGCATG	827
Oy	149	AspTYrTrsnaIAGSerGIuAlaIThrThraIa-----ProProArgProPheProIa	165
Db	828	GACTACAAACCGCACCGAGCTAACACACGCGCGCCACGCGCGCGCTGCGCGCG	887
Oy	166	LysProThrLeuProGIy-----ProProGIy	174
Db	888	CCGCGC-----CCCGGCGACACCGCGCTTCCGGCAGCGGCGACAGCGCGCGCGGG	941
Oy	175	Ala-----	175
Db	942	GCCAGGCGCCCGCACCGCGCGCGCGACAGGCGGTGCGCGCGCGGAGACCGCGCGCGCC	1001
Oy	176	ProIaIaSerGIyGIy-----GIuCYsProAlaGIyGIyProPheVal	189
Db	1002	CCAGCTCGCGCGCGCGCGGTGCGCGGAGGCGCGCGCCCTGTGCGGCGCGCGCTCCC	1061
Oy	190	-----CysLysCYeArGIuProPheValProIleLeuLYGIuSerHisPPro	205
Db	1062	TGCGAGCGCGCGGTGCGCACTGCGCGCGCGCTATGTGTGAGCGTGTCCAGGAGCGCCACCG	1122
Oy	206	LeuTYrAnLYsValArGIThGIyGIuValProIaCYsAlaValProCYsTYrGIuPro	225
Db	1122	CTTCAACAACCGCGCTCAACAGACAGCGCGCAGTCCGCTAACTGCGCGTGCCTGCGCAACAACCC	1181
Oy	226	SerPheSerAlaAsPAlaArgIuArgThnPhe	234
Db	1182	TTTTTCAGCCAGACAGCGCGCTTC	1208
<p>US-10 9</p> <p>US-10-112-944-6</p> <p>Sequence 6, Application US/10112944</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Tang, Y. Tom</p> <p>APPLICANT: Yang, Yonghong</p> <p>APPLICANT: Wang, Gezhi</p> <p>APPLICANT: Zhang, Jie</p> <p>APPLICANT: Ren, Feiyang</p> <p>APPLICANT: Xue, Aidong J.</p> <p>APPLICANT: Wang, Jiao-Rui</p> <p>APPLICANT: Wehrman, Tom</p> <p>APPLICANT: Wang, Malabika</p> <p>APPLICANT: Ghosh, Dumrui</p> <p>APPLICANT: Zhao, Qing A.</p> <p>APPLICANT: Wang, Zhiwei</p> <p>TITLE OF INVENTION: Novel Nucleic Acids and</p> <p>TITLE OF INVENTION: Secreted Polypeptides</p> <p>FILE REFERENCE: 805A</p> <p>CURRENT APPLICATION NUMBER: US/10/112,944</p> <p>CURRENT FILING DATE: 2002-03-28</p> <p>PRIOR APPLICATION NUMBER: US 09/488,725</p> <p>PRIOR FILING DATE: 2000-01-21</p> <p>PRIOR APPLICATION NUMBER: US 09/491,404</p> <p>PRIOR FILING DATE: 2000-01-25</p> <p>PRIOR APPLICATION NUMBER: US 09/496,914</p> <p>PRIOR FILING DATE: 2000-02-03</p> <p>PRIOR APPLICATION NUMBER: US 09/515,126</p> <p>PRIOR FILING DATE: 2000-02-28</p> <p>PRIOR APPLICATION NUMBER: US 09/519,705</p> <p>PRIOR FILING DATE: 2000-03-07</p> <p>PRIOR APPLICATION NUMBER: US 09/540,217</p> <p>PRIOR FILING DATE: 2000-03-31</p> <p>PRIOR APPLICATION NUMBER: US 09/552,929</p> <p>PRIOR FILING DATE: 2000-04-18</p> <p>PRIOR APPLICATION NUMBER: US 09/577,408</p>			

PRIOR FILING DATE: 2000-05-18
 NUMBER OF SEQ ID NOS: 924
 SOFTWARE: pf_fl_genes Version 5.0
 SEQ ID NO 6
 LENGTH: 3206
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (381)..(2462)
 US-10-112-944-6

Alignment Scores:
 Pred. No.: 8,53e-47 Length: 3206
 Score: 824.00 Matches: 161
 Percent Similarity: 67.66% Conservative: 21
 Best Local Similarity: 59.85% Mismatches: 39
 Query Match: 62.90% Indels: 48
 DB: Gaps: 8

US-09-847-102a-68 (1-235) x US-10-112-944-6 (1-3206)

QY 11 SerLeuLeu-----LeuLeuLeuLeuAAGInLeuValGlyArgAlaAlaAlaSer 28
 DB 411 TCGCTGCTGCGCCCTTGGCGCTGCTGCAAGCCCTTAGCGCGCTGCGCCCTCGGCC 470
 QY 29 LybAlaProValCyGInGluIleThrValProMetCyArgGlyIleGlyTyraenLeu 48
 DB 471 AAGGAGCTGGCATGCCAAGATCAACCGCTGTGTGAAGGATCGGCTACCACTAC 530
 QY 49 ThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHis 68
 DB 531 ACCTCATGCTCCCAATCAGTTCAACCAACGACGCAAGAGAGCGCGCTGAGGTGCAC 590
 QY 69 GlnPheTrpProLeuValGluIleGlnCysSerProAspLeuArgPheLeuCysThr 88
 DB 591 CAGTTTGGCGCTGCTGAGATCCAGTCTCGCCGATTCAGTTCTTCTGTCGAC 650
 QY 89 MetTyrrProIleCysLeuProAspTyrrHisIleTyrrProLeuProProCysArgSerVal 108
 DB 651 AAGTACAGCCCATCTGCTAGAGACTACCAAGAACCCCTGCGCTCGCTCGG 710
 QY 109 CysGluArgAlaLybAlaGlyCysSerProLeuMetArgGlnTyrrGlyPheAlaTrpPro 128
 DB 711 TCGGAGCGCGCAAGCGCGCTGCGCGCTCATGCGCAGTACGCGCTTGGCTGCGCC 770
 QY 129 GluArgMetSerCysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMet 148
 DB 771 GACCCCATGCTGCTGCAAGCGCTGCGCGCAAGGC---AACCTGACAGCTGTGCATG 827
 QY 149 AspTyrrAsnArgSerGluAlaThrThraAla-----ProProArgProPheProAla 165
 DB 828 GACTACAAACCGACCGAAGCTTAAACACCGCGCGCCAGCCCGCGCGCTTGGCGCG 887
 QY 166 LysProThrLeuProGly-----ProProGly 174
 DB 888 CCGCGG-----CCGCGGAGAGCGCGCTTGGCGAGCGCGCGCGCGCGCGG 941
 QY 175 Ala----- 175
 DB 942 GCCAGAGCCCGCACCGCGCGCGCGAGGCGGTGGCGCGCGAGCGCGCGCGCGCC 1001
 QY 176 ProAlaSerGlyIle-----GluCysProAlaGlyIleGlyProPheVal 189
 DB 1002 CCAAGCTCGCGCGCGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCTCC 1061
 QY 190 -----CysIleCysArgGluProPheValProIleLeuLysGluSerHisPro 205
 DB 1062 TCCGAGCCCGGTGCGAGTGCAGCGCGCTATGTAGGTGTCCAGCAGAGCGCACCG 1121
 QY 206 LeuTyrrAsnLeuValArgThrGlyIleValProAsnCysAlaValProCysTyrrGlnPro 225
 DB 1122 CTCTACACCGGCTCAAGACGAGATCGTAACTGCGCGCTGCGCGCACAAACCC 1181

QY 226 SerPheSerAlaAspGluArgThrPhe 234
 DB 1182 TTTTTCACGACGAGACGCGCGCTTC 1208

RESULT 10
 US-10-144-771-10276
 Sequence 10276, Application US/10144771
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig
 TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
 FILE REFERENCE: CLO01321
 CURRENT APPLICATION NUMBER: US/10/144,771
 CURRENT FILING DATE: 2002-05-15
 NUMBER OF SEQ ID NOS: 47235
 SEQ ID NO 10276
 LENGTH: 2058
 TYPE: DNA
 ORGANISM: HUMAN
 US-10-144-771-10276

Alignment Scores:

Pred. No.: 5.58e-47 Length: 2058
 Score: 823.50 Matches: 159
 Percent Similarity: 69.06% Conservative: 24
 Best Local Similarity: 60.00% Mismatches: 39
 Query Match: 62.86% Indels: 43
 DB: Gaps: 8

US-09-847-102a-68 (1-235) x US-10-144-771-10276 (1-2058)

QY 11 SerLeuLeu-----LeuLeuLeuLeuAAGInLeuValGlyArgAlaAlaAlaSer 28
 DB 31 TCGCTCTAGCGCGCTTGGCGCTGCTTACAGGCTCTACAGCGCGCTGCGCGCTTGGCG 90
 QY 29 LybAlaProValCyGInGluIleThrValProMetCyArgGlyIleGlyTyraenLeu 48
 DB 91 AAGGAGCTGGCGTGCACAGATCAACGCTGCTGTGCAAGGATCGGCTTACCACTAC 150
 QY 49 ThrHisMetProAsnGlnPheAsnHisAspThrGlnAspGluAlaGlyLeuGluValHis 68
 DB 151 ACTTACATGCCCAACCACTTCAACCAACGACGCAAGATGAGCGCGCTTACAGGTGCAC 210
 QY 69 GlnPheTrpProLeuValGluIleGlnCysSerProAspLeuArgPheLeuCysThr 88
 DB 211 CAGTTTGGCGCTGCTGAGATACAGTCTCCCGGACCTCAAGTTCTTCTGTGTAC 270
 QY 89 MetTyrrProIleCysLeuProAspTyrrHisIleTyrrProLeuProProCysArgSerVal 108
 DB 271 AATGACAGCCCATCTGCTGAGAGACTACAAAGAGCTTGGCGCTTGTGCTGTG 330
 QY 109 CysGluArgAlaLybAlaGlyCysSerProLeuMetArgGlnTyrrGlyPheAlaTrpPro 128
 DB 331 TGTGAACGCGCCCAAGCGCGCTGCGCGCTCATGCGCAGTACGCGCTTGGCGCT 390
 QY 129 GluArgMetSerCysAspArgLeuProValLeuGlyArgAspAlaGluValLeuCysMet 148
 DB 391 GACCCCATGCTGCTGAGATCGTGTGCGGAGCAGAGC---AACCGAGACACTGTGTGATG 447
 QY 149 AspTyrrAsnArgSerGluAlaThrThraAla-----ProProArgProPheProAla 165
 DB 448 GACTACAAACCGACCGAAGCTTCAACACGCGCGCGCCAGCCACCGCGCGCTGCTCG 507
 QY 166 LysProThrLeuProGly-----ProProGly 174
 DB 508 CCGCTCTCT---CCGCGGAGACCGCGCTTGTGAGCGCGCACAGCGCGCGCGCAGAG 564
 QY 175 Ala----- 175
 DB 565 GCCAGAGCCCGACATCGTGGCGGACAGTACGAGGCGACGCGGAGCGCGCGCTGCGCC 624
 QY 176 ProAlaSerGlyIleGlyIleCys-----ProAlaGlyIleProPheVal----- 189

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Db      625 CCTTCGGGGGGGAGAGGAGGAGCCCTGCTGGGGGGCTCTCCCTGCGAGCCGGGG 684
QY      190 CysLysCysArgGluProPheValProIleLeuLysGluSerHisProLeuTyraAsnLys 209
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      685 TGGCATGCGCGCGCGCCCATGTGAGCGTGTCCAGGAGGAGGAGCCCGCTCTCAACCCG 744
QY      210 ValArgThrGlyGlnValProAsnCySAValProCysTyGlnProSerPheSerAla 229
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      745 GTCAAAACGGGCGAGATCGCCCACTGTGCGCTGCGCCGACAAACCCCTTTTACGACAG 804
QY      230 AspGluArgThrPhe 234
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      805 GATGAGCGGCGCTTC 819

RESULT 11
US-10-144-771-12343
; Sequence 12343, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 12343
; LENGTH: 2043
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-12343

Alignment Scores:
Pred. No.: 1,976-23 Length: 2043
Score: 479.50 Matches: 110
Percent Similarity: 54.05% Conservative: 30
Best Local Similarity: 42.47% Mismatches: 79
Query Match: 36.60% Indels: 40
DB: 9 Gaps: 11

US-09-847-102a-68 (1-235) x US-10-144-771-12343 (1-2043)
QY      3 ArgProAspProSerHisProProSerLeuLeuLeuLeuLeuValGlnLeuVal 21
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      217 CGCCCTGCGCGCGAGCGCCCTGCGCGCTGCTGCGCATCTGCTGCTGCGCGCGCG 276
QY      21 1G1YARGA1A1A1A1A1A1A1A1A1A1A1A1A1A1A1A1A1A1A1A1A1A1A1A1 34
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      277 CGGACCGCGCCCACTTCCAGCGGAGAGGAGCATCTCCATCCCGAGCAGCGCTTCCGCA 336
QY      34 ngL1eThrValProMetCysArgGly1leGlyTyraSnLeuThrHisMetProAsnG1 54
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      337 GCCCATCTCATCTCCCTGCGCGAGCATCGCTCAACACCAACATCATGCGCCAACT 396
QY      54 nPheAsnHisAspThrGlnAspGlnValGluGlnValHisGlnPheThrProLeuVal 74
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      397 TCTTGCGCCACAGACAGAGAGAGCGGCGCTGAGAGTGACATGAGTTTAACTGCGTGGT 456
QY      74 1G1u1leGlnCysSerProAspLeuArgPhePheLeuCysThMetTyThrProIleCy 94
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      457 GAAAGTGCACTGTCTCCCGAGCTGCGCTTCTCTGCTGCTCATGTACGCGCGGCTGTG 516
QY      94 sleuProAspThrHisLysProLeuProProCysArgSerValCysGluArgAlaLysAl 114
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      517 CACAGTG---CTGAGACAGGAGCATCCCGCGCTGCGCTCATCTGCGAGCGCGCGCA 573
QY      114 agLysSerProLeuMetArgGlnTyGlyPheAla1TrpProGluArgMetSerCysAs 134
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      574 AGGCTCGAGGCGCTCATGAACAAGTTGCGCTTCCAAATGCGCCAGCGCTCGCGCA 633
QY      134 ArgGluProValLeuGlyArgAspAlaGluValLeuCysMetAspTyThrAsnArgSerG1 154
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      634 GCATTTCGCCCGTCACGGC-----GCGAGCAGATCTGCTGCGGAGCAACACTCGGA 687
QY      154 u-----AlaThrThrAlaProProArgProPheProAlaLysProTh 168

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Db      688 GGACGAGCTCTGCGCTACTACACACCGCGCACCTTCTGGGCTG-----CACCCGG 741
QY      168 rleuProGlyProProGlyAlaProAlaSerGlyGlyCysProAlaGlyGly----- 186
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      742 CGGGGTGACACCCCGCGCGGCTGCGGCGTGTGCTGCGACCGCGCTTACCGCACTCT 801
QY      187 -----ProPheValCysLysCysArgGluProPheValProIleLeuLysGluSerH 204
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      802 GGAGCACCTTCCACTGTC-----CGCGCTCTCAAGTG----- 838
QY      204 sProLeuTyraAsnLysValArgThrGlyGlnValProAsnCySAValProCysTyG1 224
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      839 -CGGCTCATCTCACTAAGTTTCTGGTGAGCGGAGCATGTGTGCGCGCTGCG---GA 894
QY      224 nProSer-----PheSerAlaAspGluArgThrPheAla 235
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      895 GCGCGACGCGCGCGAGCGCTCATGTCTTCTCGCAAGAGAGACTCGTTTGCC 949

RESULT 12
US-10-285-976-42
; Sequence 42, Application US/10285976
; GENERAL INFORMATION:
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Malini, Sen
; APPLICANT: Wu, Christina
; APPLICANT: Leoni, Lorenzo M.
; APPLICANT: Corr, Maripat
; APPLICANT: Carson, Dennis A.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
; FILE REFERENCE: 023070-130320US
; CURRENT APPLICATION NUMBER: US/10/285,976
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/287,995
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: WO PCT/US02/13802
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 1983
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human frizzled2 (Fzd2)
US-10-285-976-42

Alignment Scores:
Pred. No.: 2,836-23 Length: 1983
Score: 477.00 Matches: 107
Percent Similarity: 51.70% Conservative: 31
Best Local Similarity: 41.63% Mismatches: 81
Query Match: 36.41% Indels: 38
DB: 8 Gaps: 10

US-09-847-102a-68 (1-235) x US-10-285-976-42 (1-1983)
QY      3 ArgProAspProSerHisProProSerLeuLeuLeuLeuLeuValGlnLeuValGly 22
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      136 CGGCGCGGAGCGCGCTGCGCTGCTGCGCTGCTGCGCTGCTGCGCGCGCGCGG 195
QY      23 ArgAlaAlaAlaSerLysAlaProVal-----CysGlnGlu 35
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      196 CCGGCGCGAGTTCACGGGAGAGGAGCATCTTCATCCCGAGACAGCGCTTCTGCAAGCC 255
QY      36 1leThrValProMetCysArgGly1leGlyTyraSnLeuThrHisMetProAsnGlnPhe 55
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      256 ATCTCATCTCCGCTGTGACGAGCATCGCTCAACACCAACATCATGCGCAACCTTTCG 315
QY      56 AsnHisAspThrGlnAspGlnValGluGlnValHisGlnPheThrProLeuValGlu 75
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY 23 ArgAlaAlaAlaAlaSerIySAlaProVal-----CysGlnGlu 35
 Db 196 CCGGCGCCAGATTCCAAGGGGAGAAAGGCATCTCCATCCCGGACACAGGCTTCTGCGACGCC 255
 QY 36 ILeThrAlaProMetCysArgGlyIleGlyTYrAsnLeuThrHisMetProAsnGlnPhe 55
 Db 256 ATCTCCATCCCGCGCTGTCTCAGCAGCATGCTCTTACACAGACCATCATGATGCCCACTTCTG 315
 QY 56 AsnHisAspThrGlnAspGlnAlaGlyLeuGlnValHisGlnPheThrProLeuValGlu 75
 Db 316 GGCCACACGAAACGAGAGAGACGAGCGCTGAGAGTGACCAAGTTCTATCGCTGTGAG 375
 QY 76 ILleGlnCysSerProAspLeuArgPhePheLeuCYrTherMetTYrThrProIleCysLeu 95
 Db 376 GTGAGAGGCTCGCGCGAATCGCGCTCTTCTGCTGTGCATGTAAGCAGCCGTGTGACCC 435
 QY 96 ProAspTYrHisIySProLeuProProCysArgSerAlaCysGlnArgAlaIySAlaGly 115
 Db 436 GTG---CTGGAACAGGCCATCCGCGCGCTGCTTATCTGTGAGCCGCGCGCAGAGCC 492
 QY 116 CysSerProLeuMetArgGlnTYrGlyPheAlaThrProGlnArgMetSerCysAspArg 135
 Db 493 TGGCAACCCCTCATGAACAAGTTGCGTTTTCAGTGGCCGAGGCCCTGCGCTGGAGCAC 552
 QY 136 LeuProValLeuGlyArgAspAlaGlnValLeuCysMetAspTYrAsnArgSerGlu-- 154
 Db 553 TTCCCGCGCAGCGC-----GCCGAGCAGATGCTGCTGCGCCAGAACCACTCCGAGGAC 606
 QY 155 -----AlaThrThrAlaProProArgProPheProAlaIySProThrLeu 169
 Db 607 GGAAGCTCCGCGCTACTCACACCGCGCGCCCGCGGAGACTG-----CAAGCGGTGCC 660
 QY 170 ProGlyProProGlyAlaProAlaSerGlyGlyCysProAlaGlyGlu----- 186
 Db 661 GGGGGGACACCCGGGTGGCCCGGGGCGGCGCGGCTCCCGCGCTACGCCAGCCTGGAG 720
 QY 187 ---ProPheValCysIySArgGluProPheValProIleLeuIySArgSerHisPro 205
 Db 721 CACCCCTTCCACGCTCCCG-----CGCGTCTCAAGGTG-----CCA 756
 QY 206 LeuTYrAsnIySAlaGlnThrGlyGlnValProAsnCysAlaValProCYrTYrGlnPro 225
 Db 757 TCCATCTCAGCTACAGATTTCGGGCGAGCGTATGTGCTGCGCCCTCG---GAACCT 813
 QY 226 Ser-----PheSerAlaAspGlnArgThrPheAla 235
 Db 814 GCGCGCGCCGATGTTCCATGTTCTTCTCACAGAGAGAGACGCTTTCGCC 864
 RESULT 14
 US-10-170-235-33965
 Sequence 33965, Application US/10170235
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig
 TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
 FILE REFERENCE: C0001380
 CURRENT APPLICATION NUMBER: US/10/170,235
 CURRENT FILING DATE: 2003-03-17
 NUMBER OF SEQ ID NOS: 42514
 SEQ ID NO 33965
 LENGTH: 1933
 TYPE: DNA
 ORGANISM: HUMAN
 US-10-170-235-33965
 Alignment Scores:
 Pred. NO.: 5.58e-23 Length: 1933
 Score: 472.50 Matches: 108
 Percent Similarity: 54.33% Conservative: 30
 Best Local Similarity: 42.52% Mismatches: 77
 Query Match: 36.07% Indels: 39
 DB: 8 Gaps: 11

